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(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		Published <i>Without international search report and to be republished upon receipt of that report.</i>
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).		
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).		

(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

## (57) Abstract

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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COMPOUNDS FOR IMMUNOTHERAPY  
OF PROSTATE CANCER AND METHODS FOR THEIR USE

**TECHNICAL FIELD**

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

**BACKGROUND OF THE INVENTION**

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1  $\mu$ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE<sup>TM</sup> system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### Example 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and Xhol, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/Xhol site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spikc (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR  
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### Example 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun;  
Dillin, David C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.427C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTCACAG TATAACAGCT CTTTATTTCT GTGAGTTCTA CTAGGAAATC	60
ATCAAATCTG AGGGTTGTCT GGAGGACTTC AATACACETC CCCCCATAGT GAATCAGCTT	120
CCAGGGGGTC CACTCCCTCT CCTTAATTCA TCCCATCCC ATCCCCAAAGC AAACACCCTCC	180
CTTCTTGTGCT CACAGCCTTCTCTAGGCTTC CCAAGTGCCTC CAGGGACAGAG TGCGTTATGT	240
TTTCAGCTCC ATCCTTGCTG TGAGTGTCTG GTGCCCTGTG CCTCCAGCTT CTCTCAGTG	300
CTTCATGGAC AGTGTCCAGC ACATGTCACT CTCCACTCTC TGAGTGTGGA TCCACTAGTT	360
CTAGAGGGC CGCCACCGCG GTGGACCTCC AGCTTTGTG CCTTTAGTG AGGCTTAATT	420

GCGCGCTTGG CGTAATCATG GTCATAACTG TTTCCCTGTGT GAAATTGTTA TCCGCTCACA	480
ATTCACACCA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGGTGC CTAATGAGTG	540
ANCTAACTCA CATTAAATTGC GTTGGGCTCA CTGNCGGCTT TCCAGTNGGG AAAACTGTCG	600
TGCCAGCTGC ATTAATGAAT CGGCUAACGC NCAGGGAAAAA CGGGTTGCG TTTTGGGGC	660
TCTTCCGCTT CTCGCTCACT NANTOCTGCG CTCGGTCNTT CGGCTGCGGG GAACGGTATC	720
ACTCCTCAA GGNGGTATTA CGGTTATCCN NAAATNGGG GATACCCNGG AAAAAANTTT	780
AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA	814

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 816 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT TGGATGGTGG AGCACCTTTC TATACGACTT ACAGGGACAGC AGATGGGAA	60
TTCATGGCTG TTGGAGCAAT AGAACCCCCAG TTCTACCGAGC TGCTGATCAA AGGACTTGGA	120
CTAAAGTCTG ATGAACCTCC CAATCAGATC AGCATGGATG ATTGCCAGA AATGAAGAAG	180
AAGTTTGAG ATGTATTGTC AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC	240
ACAGATGCCT GTGTGACTCC GGTTCTGACT TTTGAGGAGG TTGTTCATCA TGATCACAAC	300
AAGGAACGGG GCTCGTTTAT CACCAAGTGTAG GAGCAGGACG TGAGCCCCCG CCCTGCACCT	360
CTGCTGTTAA ACACCCCAGC CATCCCTTCT TTCAAAAGGG ATCCACTAGT TCTAGAACGCG	420
GCCGCCACCG CGGTGGAGCT CCAGCTTTG TTCCCTTAG TGAGGGTTAA TTGCGCGCTT	480
GGCGTAATCA TGGTCATAGC TGTTTCTGTG TGAAATTGT TATCCGCTCA CAATTCCCCC	540
AACATACGAG CGGAAACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN	600
CATTAATTGC GTTGCCTCA CTGCCGCTT CCGAGTCGGG AAAACTGTCG TGCCACTGCN	660
TTANTGAATC NGCCACCCCC CGGGAAAAGG CGGTTGCNTT TTGGGCCTCT TCCGTTTCC	720
TCGCTCATTC ATCCTNGCNC CCGGTCTTCG GCTCCGNGA ACGGTTCACT CCTCAAAGGC	780
GGTNNTNCCGG TTATCCCCAA ACNGGGATA CCCNGA	816

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 773 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG AAGGGATGGC TGGGGTGTAAACAGCAGAG GTGCAGGGCG GGGGCTCACG	60
TCCTGCTCCT CACTGGTGAT AAACGAGCCC CGTTCCTGTGT TGTGATCATG ATGAACAAACC	120
TCCCTAAAGAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACCCAC	180
TCTGCCTTCG TCTTCTTGC AAATCATCTGC GCAAACCTCT TCTTCATTTTC TGGCCAATCA	240
TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC CANNTCCTTT GATCAGCAGC	300
TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCCATCTGC TGTCTGTAA	360
GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTC CTGAGGGGG GGCCCGGTAC	420
CCAATTGCGC CTATANTGAG TCGTATTACG CGCCCTCACT GGGCGTCGTT TTACAACGTC	480
GTGACTGGGA AAACCCCTGGG CGTTACCAAC TTAATGCGCT TGCAGCACAT CCCCCCTTCG	540
CCAGCTGGGC GTAATANCAGA AAAGGCCGC ACCGATCGCC CTTCACACAG TTGCGCACCT	600
GAATGGGNAATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCAGNGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTTGCCA GCGCCTTANC GCCCGCTCCC TTTCNCCTTT	720
CTTCCCTTCC TTTCNCNCNN CTTTCCCCCG GGGTTTCCCC CNTCAAACCC CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGACT CCTACTGAC	1	TGTGCTTCT GGTGTGGAGT CCAGGGCTG	2	TAGGAAAAGG	3
AATGGGCAGA CACAGGTGTA	4	TGCCAATGTT TCTGAAATGG	5	GTATAATTTC	6
TCGGAACACT GGCTGTCCTCT	7	GAAGACTTCT CGCTCAGTTT	8	CAGTGAGGAC	9
ACGTGGGTGA CCATGTTGTT	10	TGTGGGGTGC	11	ACACACAAAG	12
AGAGTGGACA GTGACACAAG	13	GTGGACACTC	14	TCTACAGATC	15
ACAATCCATC AGGCACACAU	16	ACTGAGGATA	17	AGCTGGAGCC	18
ACAGCAAGGA TGACNCTGTA	19	AACATAGCC	20	AGCTGTCCT	21
GNGGGCACTG GGAAGCCTAN	22	ATNAGGCCGT	23	GAGCANAAAG	24
AGAGGGAGGA TCCACTAGTT	25	410	26	AAGGGGAGGA	27
CTANAGCGGC CGCCACCGCG	28	420	29	TCCACTAGTT	30
GTGGANCTCC ANCTTTGTT	31	430	32	CCCTTTAGTG	33
GCAGCGTTGG CNTAATCATG	34	440	35	AGGGTTAATT	36
GTCATANCTN TTTCTGTGT	37	450	38	GCAGCTCACA	39
GAAATTGTTA TCGGCTCACA	40	460	41	ATTCCACACA ACATACGANO	42
CGGAAACATA AANTGAAAC	43	470	44	CTGGGGTGC	45
CTAACTCACA TTAATTGCGT	46	480	47	TAATGANTGA	48
TGCGCTCACT GCCCCTTTC	49	490	50	CTAACATCACA	51
CAATCNGGAA ACCTGTCTTG	52	500	53	CCNCTTGAT TNATGAATCN	54
GCCAACCCCC GGGGAAAGC	55	510	56	GTTTGCCTTT	57
GTTTGCCTCT CGGCTGCNGC	58	520	59	TGGGCGCTCT	60
AAACCGGGTTC ACCNCCTCCA	61	530	62	TCCGCTTCT	63
AAGGGGGTAT TCCGGTTTCC	64	540	55	CCNAATCCGG	56
CCNAATCCGG GGANANCC	65	550	56		

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT TTTTTACTGA	1	TAGATGGAAT TTATTAAGCT	2	TTTCACATGT	3	GATAGCACAT	4
AGTTTTAATT GCATCCAAAG	5	AACTCTAGCA	6	ATCAAGAATG	7	GCAGCATGTT	8
ATTTTATAAC AATCAACACG	9	TGTGGCTTTT	10	AAAATTGGT	11	TAATTTATAC	12
TGAAGTAAT CTAGCCATGC	13	TTTTAAAAAA	14	TTTCATAAGA	15	TAACTTGTCA	16
ACATTGGCA TAAACAATAA	17	TGCTTTAGGT	18	TTGGCAGTTA	19	240	250
AAAACAATTC ACAATTAAAT	21	CACTCCAAG	22	ACATACATTG	23	300	310
TAGGCCATAA TCATATACAG	24	AGCTCCTAGT	25	TACAACATTG	26	360	370
TATAAGGAAA GTTGAGTANG	27	GTTGAGTANG	28	CAGTTATTAG	29	430	440
AATAGAAATAC CTTGGCCTCT	30	AAATAACAAA	31	AAATAACAAA	32	480	490
ATGCAAATAT GTCTAGACAC	33	TACAACATTC	34	TACAACATTC	35	540	550
CATTCAAGTT TCAAAGTAGG	36	TTTTACAGTT	37	TCCAACACAT	38	600	610
AGACAGGTTT TACAGTATCA	39	TTTATTAAATG	40	TCAAGAGTTA	41	660	670
TGAAAACAAG TAGAAAATGA	43	CATTACATCC	44	TCACCAACCC	45	720	730
TGAGTTGATT TCAAGAGTTA	46	TTAGTTATATT	47	CTCAGTTATAA	48	780	790
AGTCAATATAA AGTCAATATAA	49	AGTCAATATAA	50	TTGGGTGTGC	51		
TTATTTTAAA TTAGTGCTAA	53	TTAGTGCTAA	54	TTATTTTAAA	55	834	
ATGCAATTAG TGAGAGACAAC	56	TTAGTGCTAA	57	TTAGTGCTAA	58		
AATGGTCCCC TAATGTGATT	59	TTAGTGCTAA	60	TTAGTGCTAA	61		
GATATTGGTC ATTTTACCA	61	CTNAACTTTC	62	CTNAACTTTC	63		
GCTTCTAAAT CTNAACTTTC	64	AGGCTTTTGA	65	AGGCTTTTGA	66		
ACTGGAACAT TGNAATNACAG	67	ACTGGAACAT	68	TGNATNACAG	69		
TGTTTCCANAG TTNCAACCTA	70	TGTTTCCANAG	71	TGTTTCCANAG	72		
CTGGAACATT ACAGTGTGCT	73	TTNCAACCTA	74	CTGGAACATT	75		
TGATTCAAAA TGATTCAAAA	76	ACAGTGTGCT	77	TGATTCAAAA	78		
TGTTTATTG TAAAGGTTAACC	79	TGATTCAAAA	80	TGTTTATTG	81		
ATAATTGAA ATNA	82	ATAATTGAA	83	ATAATTGAA	84		

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTTT TTTTTTTTTT AAGACCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACCACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTGGA	120
TGTAAAGTGA AATATTACTT GGCGGATGAA GCAGATACTC AGGAAACTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTTGAGG AGGGTAAAT AGAGACCCAG	300
TAAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG	360
GTGAGCTCAG GTGATTGATA CTCTGTATGC GACTAATACG CATGTTTTA GGAGTGGGAC	420
TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TCGGGGCCAC TGCCCTCCTA STTGGGGGCT	480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAATCCT GCGAAGAAAA AAACCTTCTGA	540
GGTAATAAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATGG TATATGGTTA GTGTGTTGGG	660
TTANTANGGC CTANTATGAA GAACCTTTGG ANTGGAAATTA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAAAA GCCCTGTAA NGGGTCTGGG CTNGGTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA	818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA	60
CGGGCCCTAT TTCAAAAGATT TTAGGGGAA TTAATTCTAG GACCGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTCA GAGCATTGAC CGTAGTATAC CCCCCGTCGT GTAGCGGTGA	180
AAGTGGTTG GTTAGACGT CCGGAATTG CATCTGTTT TAAGCTTAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGTCT TGTGATGTA TTATTATACN AATGGGGCT TCAATCGGGA	300
GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTCTAGG AATAATGGG	360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTNNGTTATT	600
GAATNTTNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNNTAANGG	660
CNTTATCNTN AAAGGTNATA ACCNCTCTA TNATCCCACC CAATNGNATT CCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAANNGGC CNCCCCCCG TGNANNCCNC CTTTGTTCC	780
CTTNANTGAN GGTTATTNCNCCCTNGCNTT ATCANCC	817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120

CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG	180
TARGAAAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCC CGTCCTGGGG	240
TGGGTGGCG ANGCCTGANC CCTCTTGCGT TGCTCCCCC ANGTGGCCCG CCACCCCGTC	300
AATGTGCGTG STCCAAACAC TGAGCTCTGC TGGCGGACTT CAAGGAAAC CUCACANGG	360
GGATTTTGCT CCTANANTAA GGCTCATCTG GGCTCGGCC CGCCACCTG GTTGGCCTTG	420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACGTGTCNG SACCACCTT NGGGAGTGT	480
CTCCTTACAA CCACANNATG CGCGCTCCCT CGCGAAACC ANTCCANCC TGNGAAGGAT	540
CAAGGCCTG ATCCACTNN NCTANAACCG CGCNCCNCCG CNGTGGAAACC CNCCCTNTGT	600
TCCITTTCTN TNAGGGTTAA TNNGCCCTTG GCCTTNCCAN NGTCCTNCNC NTNTTCCNNT	660
GTTNAAATTG TTANGCNCCC NCNNNTCCCN CNNCNCCNAN CCCGACCCNN ANNTTNNANN	720
NCCTGGGGT NCNNCNGAT TGACCCNNCC NCCTNTANT TGCTTNGGG NNCNNNTGCC	780
CTTTCCCTCT NGGGANNCG	799

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCCTGA CAGTGGGCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG CCCACCAAGT CGGGGGGCCG AAGCCCCAT GATCCTTACT CTATGAGCAA	180
AATCCCCCTGT GGGGGCTTCT CCTTGAAGTC CGCCANCAGG GCTCAGTCCT TGGACCCANG	240
CAGGTCACTGG GTGTTGNGNC CAACTGGGGT CCNAACGCA AAANGGCNA GGGCCTCNGN	300
CACCCATCCC ANGACCGGGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG	360
TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCNAC TCCANCTTCT NGGACGTGCG	420
CTACATACCG CGGGANTCNC NCTCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG CACCNATTCC CACNTTTNC AGNTTTCCNC NNCGNGCTTC CTTNTAAAAG	540
GGTTGANCCC CGGAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACTN CCCCCCTNATA	600
GCTGAANTCC CCATNACCCN GNCTCNATGG ANCCNCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTAA TCCCNCCCTG CNANGNNCN CCCCCNNNTCC	720
NCCCNNTNG GCNTNTNANN CNAAAAAGGC CNNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTTC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTOCC CTACACACTG CCCTCCCTCT ACCACCCGGG GAAGCAGGTG TTCTGCCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACG AGCTTCCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGTGGA GGCAGTGGCC	300
TGCTCCCACT TCCACCCGGG CTCTGCGGGG CCTCTGCCGT TGATGTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGTCTC TGCTGTCCA NGTGGCCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT CGCGCAGGCC TGGGTCTGGT	540

CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC	660
TCTGTAAAC CCCATGGGGC TCCCCTGGTGC GCCGCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCCTGGCT GAAGTGCNTA CNGNCANCT NGGGGGTNG	780
CGNSTTCCS	789

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTTAAAT AAATAAGTTA AATATTTAA TGCCCTGTGTC TCTGTGATGG CAACAGAACG	120
ACCAACAGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTTG TGCCCTCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTTAA CGAAGCTGCA GTTAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCACTGC CCAAAACCCC TTCTCTAGGT GTGTCCTAAC TAGGAGGCTA GCTGTTAAC	420
CTGAGCCTGG GTAATCCACC TGCAAGTCC CCGCATTCCA GTGCATGGAA CCCTCTGGC	480
CTCCCTGTAT AAGTCCAGAC TGAAACCCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA	540
AACTGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCANCTACG CACCTCAACA	600
GCACAGGGTG GCAGCAAAAA AACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGGCA	660
ACCCCGGCAC CCCNANGGGG GTTAACAGGA ANCNGGNAA CNTGGAACCC AATTNAGGCA	720
GGCCCNCCAC CCCNAATNTT GCTGGAAAT TTTCTCTCCC CTAAATTNTT TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTC CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTCGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCCCTC TACTTTTTGG TCGTGAGCCT TTTGCTTGGT GCAGGTTTC	120
TTGGCTGTG TGTTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCACT GTTCTCTTTG	180
AAGTANGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGGC CACAGCACTT GAGCCCTTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCCTGGAAC CATAATCTTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAG GGAAGTGCTC AGCCATTGTC GTGTACACCA AGGCAGCAC	360
AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGANGATG AAGAAGAACG TCNCAGGGC	420
ACACTTGCTC TCACTCTTAN CACCATANCA GCCCNTGAAA ACCAANANCA AAGACCACNA	480
CNCCGGCTGC GATGAAGAAA TNACCCCNCG TTGACAAACT TGCACTGGCAC TGGGANCCAC	540
AGTGGCCNA AAAATCTTCA AAAAGGATGC CCCATCNATT GACCCCCCAA ATGCCCACTG	600
CCAACAGGGG CTGCCCCACN CNCNNAAACGA TGANCCNATT GNACAAGATC TNCNTGGTCT	660
TNATNAACNT GAACCCCTGCN TNGTGGCTCC TGTTCAGGNC CNNGGCCTGA CTTCTNAANN	720
AANGAACTCN GAAGNCCCCA CNGGANANNC G	751

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGGCG	TCCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CGGGGAGCTG	TTTTGTCCTT	60
TGTGGANCT	CAGCAGTNCC	CTCTTTCAGA	ACTCANTGCG	AAGANCCCTG	AACAGGAGCC	120
AJCATGCAGT	GCTTCAGCTT	CATTAAGACG	ATGATGATCG	TCTTCATAATT	GCTCATCTT	180
CTGTCTGGTG	CACCCCTGTT	GGCAGTGGGT	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TGGGGCCACT	GTCGTCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CGGGCGTTGT	GGTCTTAGCT	CTAGGTTC	TGGGCTGCTA	TGGTGCCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	GGTGACGTT	TTCTTCATCG	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCCTGACGT	480
TGCTGCTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTGC	CAGGAANACT	TCACTCAAGT	540
GTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATTTC	600
GAAGANTCAC	CTACTTCAAA	GAAAANAGTC	CTTTTCCCDC	ATTTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGTCC	CCAAACCANA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 816 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCGCA	TAACAAACCAAC	CATAGGTAAA	GGGGGCGCAG	60	
TGTTTCGCTGA	AGGGGGTGT	GTACCCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120	
GGCAGGTCCA	CGCAGTGC	CCC	GGAAATGGA	TGCCTGGAG	CTCGTCAAAG	180	
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACCGT	CGGGGCAGTT	GGGGGTGTCT	240	
TCAACACTCCA	GGAAACTGTC	NATGCCAGCAG	CCATTGCTG	AGCGGAAC	GGTGGGCTGA	300	
CANGTGCCAG	AGCAGACTGG	ATGGGCGCTT	TCCATGN	GGGCCCTGNG	GGAAAGTCCC	360	
TGANCCCCAN	ANCTGCTCT	CAAANGCCCC	ACCTTGACACA	CCCCGACAGG	CTAGAATGGA	420	
ATCTTCTTCC	CGAAAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCN	ACAAACTCTT	480	
GCANATCTGC	TCCGN	TCNTANTACC	ANC	GTGGAA	AAGAACCCCA	540	
CAANCTTGT	TGGATNC	GCNATAATCT	NCT	NTCTG	TTGGTGGACA	600	
CTGTINNAN	TTAGNCCNTG	GTCTCTN	GTGNNCTG	AACTAATCN	CCNN	TC	660
GGGACAAGGT	AA	NT	CC	CC	CC	CC	720
CNCNCTCTA	CCCCAGAAAN	NCCGTGT	CCCCCTGGTT	TGGG	TTTT	TT	780
CACAACCCTN	CCCCACCCAC	GGGTT	GGG	CCN	CCN	NT	816

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 783 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAAACCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGAATAG	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTGCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCCCGCT	CCAACAAAGT	GGCTCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGGTG	420
TGCAAGGTGG	GCCTTTGANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCG	CAGGGCCCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTCCCTNG	AATTGTGACA	ACACCCCCCC	NTGCCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTNAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCCCG	660
CNCCTCCNTT	TTCCCCNNNT	AACAAAGGGC	NCTNGCNNTT	GAATGCCCN	AAACCNNGAA	720
TCTNCCNNNG	AAAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNAA	ANCTNCCCCC	780
CCC						783

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 801 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATIC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTTGG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCACT	GTTCTCTTG	180
AAGTAGGGT	AGTCTCTAAA	ATCCGTATAG	TTGGTGAAAC	CACAGCACTT	GAGCCCTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTTGG	TGTACACCAA	GGCGACCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAAA	GACCACAAAG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGCCCCGAAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AAACACCCANA	TGCCCACACTGC	600
CNACAGGGCT	GCNCCNCNCN	GAAAGAATGA	GCCATTGAAG	AAGGATCNTC	NTGGTCTTAA	660
TGAACGTAAA	CCNTGCTATGG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCG	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCN	G				801

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 740 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGGCCA	GGCGTCCCTC	TGCCTGCCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGTCTCA	GCTTCATTAA	GACCATGATG	ATCTCTTCA	ATTTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGTCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTCGGGC	CACTGTCGTC	CAGTGCATG	CAGTTGTCA	ACGTGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTGGT	TTCCCTGGGCT	GCTATGGTGC	360

TAAGACGGAG	ASCAAATGTG	CCCTCGTGA	GTTCTTCITC	ATCTCTCTC	TGATCTTCAT	420
TGCTGAAGTT	GCAGCTGCTG	GGGTGCGCTT	GGTGTACACI	ACAATGGCTG	AACCATTCT	480
CACGTTGCTC	CTANTGCTC	CAATCAANAA	ACATTATGGG	TTCCCAGGA	AAATTCACTC	540
AANTNTGGAA	CACCNCGATG	AAAAAGGCTC	CAATITCTGN	TGGCTTCCCC	AACTATAACCG	600
GAATTTGAA	AGANTCNECC	TACTTCAAA	AAAAAANANT	TGCCTTNCC	CCNNTTCTGT	660
TGCAATGAAA	ACNTCCAAAN	AGNGCGAATN	AAAACCTGCC	CNNNCAAAAAA	GGNTCNCAAA	720
CAAAAAAANT	NNAAGGGTTN					740

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGGTG	CGCTGGTCCA	GNGNAGGCCAC	GAAGCACGTC	AGCATACACA	GCCTCAATCA	60
CAAGGTCTTC	CAGCTGCCGC	ACATTACGCA	GGGCAAGAGC	CTCCAGCAAC	ACTGCATATG	120
GGATACACTT	TACTTAGCA	CCCAGGGTGA	CAACTGAGAG	GTGTCGAAGC	TTATTCTTCT	180
GAGCCTCTGT	TAGTGGAGGA	AGATTCCGGG	CTTCAGCTAA	GTAGTCAGCG	TATGTCCCAT	240
AAGCAAACAC	TGTGAGCAGC	CGGAAGGTAG	AGGCAAAGTC	ACTCTCAGCC	AGCTCTCTAA	300
CATTGGGCAT	GTCCAGCAGT	TCTCCAAACA	CGTAGACACC	AGNGGCTCTC	AGCACCTGAT	360
GGATGAGTGT	GGCCAGCGCT	GCCCCCTTG	CCGACTTGGC	TAGGAGCAGA	AATTGCTCCT	420
GGTTCTGCC	TGTACACCTTC	ACTTCCGCAC	TCATCACTGC	ACTGAGTGTG	GGGGACTTGC	480
GCTCAGGATG	TCCAGAGACG	TGGTTCCGCC	CCCTCNCTTA	ATGACACCGN	CCANNCAACC	540
GTCGGCTCCC	GCCGANTGNG	TTCGTCGTNC	CTGGGTCAAG	GTCGCTGGC	CNCTACTTGC	600
AANCTTCGTC	NGGCCATGG	AATTCAACCAC	ACCGGAACTN	GTANGATCCA	CTNNNTCTAT	660
AACCGGNCGC	CACCGCNNT	GGAACCTCAC	TCTTNNTNCC	TTIACTTGAG	GGTTAAGGTC	720
ACCCTTNNCG	TTACCTTGGT	CCAAACCNNT	CCNTGTGTG	ANATNGTNAA	TCNGGNCCNA	780
TNCCANCCNC	ATANGAAGCC	NG				802

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC	AGGTNACGGG	CCGCNAANCC	TGACCCNAGG	TANCANAANG	CAGNCNGCGG	60
GAGCCCACCG	TCACGGGNG	GNGTCTTTAT	NGGAGGGGGC	GGAGCCACAT	CNCTGGACNT	120
CNTGACCCCA	ACTCCCCNCC	NCNCANTGCA	GTGATGACTG	CAGAACTGAA	GGTNACGTGG	180
CAGGAACCAA	GANCAAANNC	TGCTCCNNNC	CAAGTCGGCN	NAGGGGGCGG	GGCTGGCCAC	240
GCNCATCCNT	CNAGTGTGN	AAAGCCCCNN	CCTGTCTACT	TGTTTGGAGA	ACNGCENNNGA	300
CATGCCAGN	GTTANATAAC	NGGCNGAGAG	TNANTTGCC	TCTCCCTTCC	GGCTGCGCAN	360
CGNGTNTGCT	TAGNGGACAT	AACCTGACTA	CTTAACGTAA	CCCNNGAATC	TNCCNCCCC	420
CCACTAAGCT	CAGAACAAAA	AACTTCGACA	CCACTCANTT	GTCACCTGNC	TGCTCAACTA	480
AAAGTGTACCC	CATNCCCAAT	GTNTGCTNGA	NGCTCTGNCC	TGCNTTANGT	TCGGTCTGG	540
GAAGACCTAT	CAATTNAAGC	TATGTTCTG	ACTGCCTCTT	GCTCCCTGNA	ACAANCNACC	600
CNNCNNTCCA	AGGGGGGGNC	GGCCCCCAAT	CCCCCUCAU	NTNAATTNAN	TTTANCCCN	660
CCCCCNGGCC	CGGCCCTTTA	CNANCNTCNN	NNACNGGGNA	AAACCNNNNGC	TTTNCCCAAC	720
NNAATCCNCC	T					731

## (2) INFORMATION FOR SEQ ID NO:20.

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20.

TTTTTTTTT TTTTTTTTT TAAAAACCCC CTCCATTNAA TGAAAACCTTC CGAAATTGTC	60
CAACCCCCCTC NTCCAATNN CCNTTTCGG GNNGGGGTTG CAAACCCAAAN TTANNTTG	120
ANNTTAAATT AAATTTNNNT TGNGGGNNNA ANCCNAATGT NANGAAAGTT NAACCCANTA	180
TNANCTTNAA TNCTGGAAA CCNGTNGNTT CCAAAATNT TTAACCCTTA ANTCCCTCG	240
AAATNGTTNA NGGAAAACCC AANTTCTCNT AAGGTTGTT GAAGGNTNAA TNAAAANCCC	300
NNCCAATTGT TTTTNGCCAC GCCTGAATTA ATTGGNTTCC GNTGTTTCC NTTAAAANAA	360
GGNNANCCCC GGTTANTNAA TCCCCCNNC CCCAATTATA CCGANTTTT TTNGAATTGG	420
GANCCNCGG GAATTAACGG GGNNNNTCCC TTTGGGGGG CNGGNCCCC CCCNCNTCGGG	480
GGTTNGGGNC AGGNCCNAAT TGTTTAAGGG TCCGAAAAAT CCCTCCNAGA AAAAAANCTC	540
CCAGGNTGAG NNTNGGGTTT NCCCCCCCCC CANGGCCCT CTCGNANAGT TGGGGTTTGG	600
GGGGCCTGGG ATTTNTTTC CCCTNTTNCC TCCCCCCCC CCGGGGANAG AGGTTNGNCT	660
TTTGNTCNNC GGCCCCNCCN AAGANTTTN CCGANTTNAN TTAAATCCNT GCCTNGGCGA	720
AGTCCNTTGN AGGGNTAAAN GGCCCCCTNN CGGG	754

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT GACCCNAAC NNNGGACCNC TCANCCGGNC NNNCNACCNC CGGCCNATCA	60
NNGTNAGNNC ACTNCNNTTN NATCACNCCC CNCCNACTAC GCCCNCNANC CNACGCNCTA	120
NNCANATNCC ACTGAANGCG CGANGTNGAN NGAGAAANCT NATACCAAG NCACCAACN	180
CCAGCTGTCC NANAANGCCT NNATACNGG NNNATCCAAT NTGNANCCTC CNAAGTATTN	240
NNCNANAT GATTTCCCTN ANCCGATTAC CCNTNCCCCC TANCCCTCC CCCCCAACNA	300
CGAAGGCNCT GGNCCNAAGG NNNGCNCNCC CCGCTAGNTC CCCNNCAAGT CNCNCNCCTA	360
AACTCANCN NATTACNCGC TTCNTGAGTA TCACTCCCCG AATCTCACCC TACTCAACTC	420
AAAAANATCN GATACAAAAT AATNCAAGCC TGNTTATNAC ACTNTGACTG GGTCTCTATT	480
TTAGNGGTCC NTNAANCNTC CTAATACTTC CAGTCTNCCT TCNCCAATTTC CCNAANGGCT	540
CTTTCNGACA GCATNTTTG GTTCCCNNTT GGGTTCTTAN NGAATTGCCC TTCNTNGAAC	600
GGGCTCNCTC TTTCCTTCGG TTANCCTGGN TTCNNCCGGC CAGTTATTAT TTCCCNNTTT	660
AAATTCTNCC CNTTANTTT TGGCNNTCNA AACCCCCGGC CTTGAAAACG GCCCCCTGGT	720
AAAAGGTTGT TTTGAAAAAA TTTTGTGTTT GTTCC	755

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTTT	TTTTTANGTG	TNGTGTGCA	GGTAGAGGGGT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGAOC	CGANTTCTAG	GANNNCCTT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNGAT	NNTGCTAGGG	TGNNCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCT	CACCACTTC	GGCGGCCCCG	NGN2GGGGCC	CGGGTCATTN	240
GNNTTAAACCN	CACTNNCNA	NEGGTTTCEN	NCCCCNNNG	AJJENGSGGA	TCCCCGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNOC	CTTTAACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCTTCANT	NNGGGGACT	GCNANNNGCT	CGTTNTJNG	420
NNACCCNN	GGGTNCTCG	GTTGEGANT	CNACCGNANG	CGANGGATTC	CNAAGGAAGG	480
TGCGTTNTTG	GGCCCTACCC	TTCGCTNCGG	NNCACGCTT	CGACNANGA	NCCGCTCCG	540
CNCNNCGNG	CCCTCNCCTCG	CAACACCGC	NCTCNCNGT	NCGNNNNCCC	CCCCACCCG	600
NCCCTCNC	NGNCGNANCN	CTCCNCNC	GTCTCANNCA	CCACCCCGCC	CGCCCAAGGC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNTC	GCNCGGCGN	CGNCNCNCCT	CGCCNCNGAA	720
CTNCNTCNG	CCANTNNCGC	TCAANCNNA	CNAAAAGGGG	CTGCGCGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCCGN	CTTCNACCC	ANGNNNTCCN	CGAGGACACN	NNACCCCGC	840
NNCANCAGGG						845

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTCGCTC	GNACTCGTGC	GCCTCGCTNE	TETTTTCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNA	AGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNA	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAAACNNG	AGAACCAANG	180
NGGGAATCG	TAATNAGGCG	TGGCGCCGCCA	ATNTGTCNN	GTGTTATTNTN	CCAGCNCNTC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTCGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCNC	CCGCACCAACC	360
NANNGCNCGC	NCCCCGNCT	CTTCGCCNCC	CTGTCCTNTN	CCCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCCTG	480
TGGGNNNGCG	TCTGCNCCCG	GTTCCTTCNN	NCNNCTTCCA	CGATCTTCNT	TACNGGTTCT	540
CCNGCCNTC	TCNNNCACNC	CCTGGGACGGC	TNTCCTNTGC	CCCCCTTNAC	CCCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTTCNA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGCN	GTCANCCNAG	SGAAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGGNGANGTC	720
CGAANANTCC	TCNCNTCAN	CNCTACCCCT	CGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNC2CCNCT	CGCTGCANTG	TNCTCTGCTC	840
TNACCNNPAC	GANTNTTCGN	CNCCCTCTTT	CC			872

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 815 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC	TTGAGTATTC	TATAGNGTCA	CCTAAATANC	TIGGCNTAAT	CATGGTCNTA	60
NCTGNCTTCC	TGTGTCAAAT	GTATACNAAN	TANATATGAA	TCTNATNTGA	CAAGANNGTA	120

TCNTNCATTA	GTAACAANTG	TNNTGTCCAT	CCTGTCNGAN	CANATTCCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGAA	NTCNNTNNN	NCACNNCAT	CTATCNTNCC	240
GCNCCTGAC	TGGNAGAGAT	GGATNANTTC	TNNTNTGACC	NACATGTTCA	TCTTGGATTN	300
AANANCCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTGCGTC	AGANNCATCA	AACNTGGAA	ACCGGONCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCCTCC	AGGNTTNACC	ATCCCTTCNC	AGCGCCCCCT	TTNGTGCCTT	ANAGNGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCGC	AGNCCANCCG	CAATTNGGCA	CAATGTCGNC	540
GAACCCCCTA	GGGGGANTNA	TNCAAANCCC	CACGATTGTC	CNCNCANGAA	ATCCCNANC	600
CCCNCCCTAC	CCNNCTTGG	GACNGTGAACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCCNTGGGG	GGGTGAANCT	CNGNNTCANC	CNGNCGAGGN	NTCGNAAGGA	720
ACCGGNCTN	GGNC3AANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCTCNCCA	780
NCCNACNGNT	AGNTCCCCCC	CNNGGTNCCG	AANGG			815

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	GCGTACTCCA	AAAGATTCAAGG	TTTACTCAGC	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATT	CCTGAATTGC	TATGTGTCTG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATGAAAAAG	TGGGACATTC	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTT	CTATCTNTG	TACTACACTG	AATTCCACCC	CACTGAAAAA	GATGAGTATG	300
CCTGCCGTG	GAACCATGTG	ACTTTGTAC	AGCCCAAGAT	AGTTAAGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTITGAAGAT	GCCGATTTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGC	GCNTTTAAAT	ANTGATATGC	NTATACACCC	TACCCCTTAT	GNCCCCAAAT	480
TGTAGGGGTT	ACATNANTGT	TNCNTNGGA	CATGATCTTC	CTTTATAANT	CCNCCNTTCG	540
AATTGCCCGT	CNCCCNNGTTN	NGAATGTTTC	CNNAACCACG	GTGGCTCCC	CCAGGTCNCC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTNCAA	GGTTGGGGGA	ACCNAAAATT	TNCNTNTGC	660
CCNCCCNCA	CNNTCTTGNG	NNNCNANTTT	GGAACCCCTC	CNATTCCCCT	TGGCCTCNNA	720
NCCTNNCTA	ANAAAACCTN	AAANCNTNGC	NAAANNTTTN	ACTTCCCCCC	TTACC	775

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAAATCT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NTCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTTCTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCAGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CCNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCTCTACCTG	ACNACCAGNG	ACNNNNAACT	GCNGCCTGGG	GACAGCNCTG	GGANCAGCTA	420
ACNNAGCACT	CACCTGCCCC	CCCATGGCCG	TNCGNNTCCC	TGGTCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGG	NACCAAGGGA	NCCCCCTCCT	CCANCTGTGA	AGGAAAANN	540
GATGGAATT	TNCCTTCCG	GCCNNTCCCC	TCTTCCTTTA	CACGCCCT	NNTACTCN	600

TCCCTCTNTT	NTCCTGNCNC	ACTTTTNACC	CNNNNATTTC	CCTTNATTGA	TGGANNCTN	660
GANATTCCAC	TNNCGGCTNC	CNTCNATCNG	NAANACAAA	NACTNTCTNA	CCTNGGGAT	720
GGGNNICCTTG	NTCATGCTCT	CTTTTTENCT	ACCNCNNNTT	CTTGTGCTGT	CCTTNGATCA	780
TCCAACCNTC	GNTGGCCNTN	CCCCUCNNN	CCCTTINCCG			810

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTGC	TCTCAGGGA	CCTCTGACTG	CTCTGGGCCA	AAGAAATCTCT	60
TGTTTCTTCT	CGAGCCCCA	GGCAGGGTG	ATTCAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CAAGGGGA	AATAGGGTGT	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCCTGC	CAGCCCCCTGC	CATGAGCTCT	GGGCTGGGTC	240
TCCGCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGCG	CCACACTGGC	300
TTCTTCTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTGC	TGTCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	CTTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGCCTN	GGCCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANTTCNNNNNA	ACCNGCTTNC	CNTCNCTCTC	CCNTANCCCG	CCNGGGAAANC	540
CTCCTTTGCC	CTNACCCANG	CCCNNAACCG	CCCNNTNCTN	GGGGGGCNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCTN	TNCCTCGTCC	CNNCNNGCN	NNGCANNTTC	NCNGTCCNN	660
TNNCTCTCN	NGNTTCGNAA	NGNTCNCTN	TNNNNNGNCN	NGNTNNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNNTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNTNNNN	TCTNCNCNGC	780
CCNNNCCCCC	NGNATTAAGG	CCTCCNNCT	CCGGCCNC			818

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAANGG	GGGAGGGTGTG	60
TCCCAACATG	ANGGTGNNGT	TCTCTTTG	ANGAGGGTTG	NGTTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNNAAGGN	TTTNAGGGAT	TTTCGGCTC	TTATCAGTAT	180
NTANATTCT	GTNAATCGGA	AAATNATNTT	TCCNCNGAA	AATNTTGTCT	CCATCCGNA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGN	CNGCCANGT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGAN	TNCAAATGAA	AACCTNMCAS	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCT	TGCGCCTNTG	ACTCTGNNG	AGCCCAATAC	CCNNNGNAT	GTCNCNCNGN	420
NNNGCGNCNC	TGAAANNNNC	TCGNGGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAGCNN	480
CGTTTCNCAT	NAAGGCACCT	TNGCCTCATC	CAACCNCTNG	CCCTCNNA	TTTNGCCGTC	540
NGGTTCNCT	ACGCTNNNTG	CNCCTNNNT	GANATTTC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGTA	GGCNCTTNTC	TTTNACNN	GNGGTNTACT	AATCNNCTNC	ACGCNTNCNT	660
TCTCNACCCC	CCCCUTTTT	CAATCCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGG	720
NNNCCCANNC	C					731

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNT	120
ATNTNTACNC	TCATANNCT	CNNNACCCAC	TCCCTCTAA	CCCNTACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACCN	GTGGGCNAC	CNCNNGNATT	CTCNATCTCC	240
TCCATCATNTN	GCCTANANTA	NGTNCATACU	CTATACUTAC	NCCAATGCTA	NNNCTAACNC	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTNC	ATNANCTCT	AATTTGAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TCNCACCAACC	NTTNCCCTCG	ATCCCCNNAC	AACCCCCCTC	480
CCAANTACCC	NCCACCTGAC	NCTTAACCCN	CACCATCCCC	GCAAGCCNAN	GGNCATTAN	540
CCACTGGAAAT	CACNAATNGGA	NAAAAAAAAC	CCNAACTCTC	TANCNCCNAT	CTCCCTAACNA	600
AATNCTCCTN	NAATTTACTN	NCANTNCCAT	CAANCCACN	TGAAACNNAA	CCCCCTGTTT	660
TANATCCCTT	CTTCGAAAAA	CCNACCCCTT	ANNNCCCAAC	CTTNGGGCC	CCCCCNCTNC	720
CCNAATGAAG	GNCNCCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGNCCCTT	NCCCNNGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 787 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCAGA	300
CCCATGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCGGTGGGA	TCCACTANTT	CTANAACCGN	CGCCACCCNG	GTGGGAGCTC	CAGCTTTGT	420
TCCCNNTAAT	GAAGGTTAAT	TGNCNCCTG	CGCTAACAT	NGTCANAAC	TNTTTCCCTGT	480
GTGAAATTGT	TTNTCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTTCCN	TTCNGGAAAA	CTGTCNTCCC	CTGCNTTNN	GAATCGGCCA	CCCCCCNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCCT	CCNCTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTCGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 799 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31.

TTTTTTTTTT	TTTTTTTGGG	GATGTTACTG	TTTAAITGCA	GGACGTCGGC	GTCTGCTGAC	60
CATGTTACCG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCACAGCGC	OCTGCTGAGC	120
AAACAAAGCA	TCTTGCACCC	TTTCTCTGTCT	GTCTCTGGC	GCAGGACACAT	GGGGAGGCC	180
CCGGCAGGGT	GGGGGCCACC	AGTCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGCGTG	240
GTGGCTGGTN	CNAATGGCT	GNCA-TANATE	CCTACGATTC	TTGACACCTG	GATTCACCCA	300
GGGGACCTT	TGTTCTCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANITCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCTNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GGCCACCTCT	CCNTPCNAAN	AGTAATTCA	CCCGGCCCCN	CONTCTNITG	480
CCIPGGGGCGT	TAANTACCCA	CAJOGGAACI	CANTTANTIA	TICATCTTNG	GNTGGGCTTG	540
NTNATCNCN	CTGGAANGG	CCAAAGTTGAA	AGGCCAEGC	GTNCGCONTC	CCCATAGNAN	600
NTTTTNNCNT	CANCTAATGC	CCCCCNGGC	AACNATCCAA	TCCCGGCCCCN	TGGGGGCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNNCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNC	CCCCACGCA	GAACANAAGG	NTNGAGCNC	CCGANNNNNN	NGGTNNNCAC	780
CTGGCCUCGU	UNNNNNNN					793

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTGGTNCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGGACAC	AAACAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCCGCGGCG	GGGGCGGGCG	CCCTAACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGT	TGATNTTCCT	CTGGAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTNN	AATTCACCG	GGCACAAATGC	GGTGCANCC	CCTCACCA	300
NATTAGGAAT	AGTGGTNTTA	CCCNCCNCG	TTGGCNACT	CCCTNTGGAA	ACCACTNTC	360
GCGGCTCCGG	CATCTGGTCT	TAACCTTGC	AAACNCTGGG	GGCCCTCTTT	TGGTTANTNT	420
NCCNGCACA	ATCATNACTC	AGACTGGCNC	GGGCTGGCC	AAAAAAANCN	CCCCAAACC	480
GGNCCATGTC	TTNNGGGGT	TGCTGCNATN	TNCAATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTNGGGCCCN	AAAAAAANCT	CCGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCCCTGGCC	CCCCAAATCCT	CCCCCCCNTT	NCTGGCTTTC	GAACCCACG	CCTCTNNCTT	660
TGGNNGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNCA	CCATCCCCC	NNGNNAAGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	CTTGGATGCT	CCAGCACCTT	TCTATACCGAC	TTACAGGAACA	GGAGATGGGG	60
AATTCAATGC	TGTGGAGCA	ATANAACCCC	AGTTCTACGA	GTGCTGATC	AAAGGAATTG	120
GACTAAAGTC	TGATGAACTT	CCCAATCAGA	TGAGCATGGA	TTATGGGCCA	GAAATCAANA	180
AGAAGTTTGC	AGATGTTATTT	SCAAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTCAGT	CCGTTCTGA	CTTTGAGGA	GGTTGTTCAT	CATGATCACA	300

ACAANGAACG	GGGCTCGTTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCA	GCCATCCCTT	CTTTCAAAG	GGATCCACTA	CTTCTAGAGC	420
GCNCGCCACC	GCGGTGGAGC	TCCAGCTTT	CTTCCCTTTA	CTGACCGCTTA	ATTGCCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTTG	TGTGAATIG	TTATCCGCTC	ACAATTCCAC	540
ACAACATAACG	ANCCGGAAGC	ATNAAATTAA	AAAGCCTGGN	GGTNGCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCCCT	660
CCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTTCGG	CTTGGGGCNA	780
ACGGTATCNA	CCF					793

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGCGCGACCG	GCATGTACGA	CCAACTCAAG	CCCGACTGGA	ACCCTAAAAC	CCCCAATCTT	60
ANCAAGTGCG	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAAACAG	CAGCTAATTC	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	CCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CACCTCTTGC	CCCTCAACCT	CCTCTTCTG	CTGTCCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TGNACCACCA	420
GTGTCTTGG	GCAATACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCTTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCGGG	600
ATNCNCTAGT	NCTAGAATCG	GCCCGCCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
ATTNTTAAC	CCCCCACAAT	TCCACGCCNA	CATTNG			756

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	CCTGTNTTTA	AGTTGCTCAG	TCTGCCGTC	120
TAGTCAGACA	CNCTCTTGGG	AAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNNG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGAACCTC	CCCTTCAAAG	TTGTCGGGC	CTTCATCAA	300
CTTCTNNAAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCGCAAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCONTCCNNG	CAGGGTTGGT	GGCANNCCGG	GCCCNCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGGCCA	TTCTGGATT	720
NCCNAACTTT	TTCCTCCCC	CNCCCCNCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780

GCTNTTGGCC ANTCCCCCTGGS GGGCNTNTAN CNCCCCCTNT SGTCCONTNG CGCC 334

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGC	CCGTTTCCA	TGACNAAGGC	TCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTGC	ACCCCCTGTA	180
GGAAACCCCT	CCCTTCTAAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGCTTT	GTGTTTACT	240
AATGGAAAAAA	AAAATAAA	AANAGGTTTT	GTTCTCATGG	CTGCCACCG	CAGCCTGGCA	300
CTAAACACNC	CCAGCGCTCA	CTTCTGCTTG	GANAATATT	CTTGTCTTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTTECAC	CCAGCTGGC	NCCTTCCCG	CATNTTGTG	420
ANTGANCTGG	AAGGGCTGAA	NETTAGTCTC	CAAAAGTCTC	NGCCCACAAAG	ACCGGCCACC	480
AGGGGANCTC	NTTTNCAGT	GATCTGCCAA	ANANTACCCN	TATCATCNNT	CAATAAAAAC	540
GCCCCCTGAAC	GANATGCTTC	CANCANCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAG	GAATGTTCT	GGGTCCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAN	TGANATCCCC	NGAAGCACCC	TNCCCCTGGC	720
ATTTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCNAAN	780
GNGAACTCA	AGAACGCTCN	NGAAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGT	CGCTGAAGGG	GTTGTAGTAC	CAGCGCGGGA	TGCTCTCCTT	GCAGAGTCCT	120
GTGTCTGGCA	GGTCACGCA	ATGCCCTTG	TCACTGGGG	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCCTCG	AAGCNTCCGG	GCAGTTGGG	240
GTGTCGTAC	ACTCCACTAA	ACTGTGATN	CANCAAGCCC	TTGCTGCAGC	GGAACTGGT	300
GGGCTGACAG	GTGCGAGAAC	ACACTGGATN	GGCCTTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCCTNANC	CAAACAGCCT	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGCAAATC	TGCTCCGTGG	GGGTCAATNNN	TACCAAGGT	GGGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTTGAATGC	NAAGGNAATA	ATCCCTCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAAC	GTTAACNTTG	GGCCGNGTTC	CNCTNGGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAAA	GGTANGTGCC	TTCCTTGAAT	CCCCAAANTT	CCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAAATCG	TNTTCCCCCC	CCNTANGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAATT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CGGGGGGGG	120
CAAATTAAATT	TTGGANTTTA	AATTAAATNT	TNATTNGGG	AANAANCAA	180
AATTAAACCC	ATTATNAACT	TAAATNCCTN	GAAACCCTNG	GNTTCCAAAA	240
CTTAATCCTC	TCCGAAATTG	NTAANGAAA	ACCAAATTCTN	CCTAAGGCIN	300
NGATTTAAC	CCCCTTNANT	TNTTTTNACC	CNNGNCTNAA	NTATTNGNT	360
TCCTNTTAAN	CNTNGGTAAC	TCCCGNTAAT	CAANNCCCT	AANCCAATT	420
TTTTTGAATT	GGAAATTCCN	NGGGAAATTNA	CGGGGTTTT	TCCCNNTTGG	480
CCCNCNTTCG	GGGTTTGGGN	NTAGGTTGAA	TTTTTNNANG	NCCCCAAAAA	540
AAAAAACTCC	CAAGNNTTAA	TTNGAATNTC	CCCCTTCCCA	GGCCTTTGG	600
TTTNTGGGGG	CCNGGGANTT	CNTTCCCCCN	TTNCCNCCTC	CCCCCNGGT	660
NGNNNTTGCT	TTTGGGCC	CTTNANGAC	CTTCCGGATN	GAAATTAAAT	720
GGCG					724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT	TTTTCTTTG	CTCACATT	ATTTTATTT	TGATTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTTCAT	TTGTTTCTTT	TATTTCATTT	TATTTGTTG	CTGCTGCTGT	120
TTTATTATT	TTTACTGAAA	GTGAGAGGGG	ACTTTTG	CCTTTTTCC	TTTTTCTGTA	180
GGCCGCCTTA	AGCTTCTAA	ATTGGAACA	TCTAAGCAAG	CTGAANGGAA	AAGGGGGTTT	240
CGCAAAATCA	CTCGGGGAA	NGGAAAGGTT	GCTTGTTAA	TCATGCCCTA	TGGTGGGTGA	300
TTAACTGCTT	GTACAATTAC	NTTCACTTT	TAATTAATTG	TGCTNAANGC	TTTAATTANA	360
CTTGGGGGTT	CCCTCCCCAN	ACCAACCCN	CTGACAAAAA	GTGCCNGCCC	TCAAATNATG	420
TCCCCGCNN	CNTGAAACA	CACNGCNGAA	NGTTCTCATT	NTCCCN	CAGGTNAAAA	480
TGAAGGGTTA	CCATNTTAA	CNCCACCTCC	ACNTGGCNNN	GCCTGAATCC	TCNAAAANCN	540
CCCTCAANCN	AATTNCTNNG	CCCCGGTCNC	GCNTNNGTCC	CNCCGGGCT	CCGGGAANTN	600
CACCCCNNGA	ANNCNNNNC	NAACNAAATT	CGAAAATAT	TCCCNTCNC	TCAATTCCCC	660
CNNAGACTNT	CCTCNCCNAN	CNCAATTTC	TTTNNTCAC	GAACNCNNC	CNNAAAATGN	720
NNNNCNCTC	CNCTNGTCCN	NAATCNCCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTT	CTGTAAGATC	AGGTGTTCT	CCCTCGTAGG	TTTAGAGGAA	ACACCCTCAT	60
AGATGAAAAC	CCCCCGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGGG	GTAGGAGGGG	120
CGCCCTATGC	ACAGCTGGGC	CCTTGAGACA	GCAGGGCTTC	GATGTCAGGC	TCGATGTCAA	180

TGGCTGGAA	GCGGGGGCTG	TACCTGGCTA	GGGGCACACC	STCAGGGCCC	ACCAGGAACT	240
TCTCAAAGTT	CGAGGCAACN	TCGTTGGCAC	ACACCGGAGA	CTAGGTGATN	AGCTTGGGT	300
CGGTATAAN	CGGGGTGGCG	TGTCGCGTGC	GACCTGGCAG	CCCTCCCCG	AGGAAGCCNA	360
A1AAAAGGTG	CGGGGGCGA	CGGTTTACNT	CGCACTTTC	NAANACCATG	ANGTTGGGT	420
CNAACCCACC	ACGANNCTGG	ACTTCGTTGA	NGGAATTCC	AAATCTCTTC	GNTCTTGGGC	480
TTCTNCTGAT	GGCTTANCTG	GTTGCCENGN	ATGCCAANCA	NCCCCAANCC	CGGGGGTCC	540
AAANCACCCN	CCTCCTCNNT	TCATCTGGGT	TNTTNTCC	GGACENTGGT	TCTCTCAAG	600
GGANCCATA	TCTCNACCT	TACTCAACNT	NCCCCCCNT	GNNAACCCANC	CTTCTANNGN	660
TTCCCNCCCG	NGCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CTTCCCCCCC	720
TNCCTATCT	GNACCCCN	TTTGTCTCAN	TNT			753

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATTT	ATATACATAT	ATGTTCTCAG	TATTTGGGA	CCCTTTCCAC	120
TTCCTTAAAC	CTTGTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTGAA	GTCTACATTC	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTCAGAG	GTATTTCAT	300
TTTACTTT	TGATTAATTG	TGTTTATAT	ATTAGGGTAG	T		341

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTTCAAACA	TTCTAAATAA	ATAATTTCA	GTGGCTTCAT	A		101

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT	120
TCAGATGCCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAAACCCA	180
CCTCTTGAGA GGTCACTAAA GAGGACTTAA TATTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTCTCT	60
GATTATTTGG TGTGTGTTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC	120
CTCTCCATCC TCAGGGCATTC TTCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTGTAG TAATATCTCA TAGCTCGCT GAGCTTTCA TAGGTCAATGC	240
TGCTGTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAAATAGT TCTNGTCTTT CCAGGTGTTC ATGATGGAAG	600
GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTTGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGGCCGGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCCCGTTG ATGTCGAACT	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCCACACCTG GT	852

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCACTGCG	180

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT 234

## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATT CACAGTTAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGAAAATCA ATTTAATGT GAATTGCACA TTATCCTTA	240
AAAGCTTCA AAANAAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAN AACTGAAGGG CANAAAGAAAT TAATTTCAC TTCATGTAAAC NCACCCANAT	360
TTACAATGCC TAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTC	420
TGGCTCTAA TCTGCCCTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAAT TTTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120
GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AAACATCAAAG AAAGGAAGGT GGCgtCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CCTCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCCACC CTCTGCTGAT CCTCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGT ATATTCCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTG CTCCCTGCAG CCTGTCAAA TCCCACACTAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGT TCTGCTAAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTGTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA	GTCTAGGGGA	CACACGACTC	TGGGGTCACG	GGGCCGACAC	ACTTGCACGG	60
CGGGAAGGAA	AGGCAGAGAA	GTGACAACCGT	CAGGGGGAAA	TGACAGAAAG	GAAAATCAAG	120
GCCTTGCAAG	STCAGAAAGG	GGACTCAGGG	CTTCCACUAC	AGCCCTGCC	CACTTGGCCA	180
CCTCCCTTTT	GGGACCAGCA	ATGT				264

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA	CATTTATCTT	ATAACAAAAA	TTTGATAGTT	TTAAAGGTTA	GTATTGTGTA	60
GGGTATTTTC	CAAAAGACTA	AAGAGATAAC	TCAGGTAAAA	AGTTAGAAAT	GTATAAAACA	120
CCATCAGACA	GGTTTTTAAA	AAACAAACATA	TTACAAAATT	AGACAATCAT	CCTTAAAAAA	180
AAAACCTCTT	GTATCAAATT	CTTTGTTCA	AAATGACTGA	CTTAANTATT	TTTAAATATT	240
TCANAAACAC	TTCCTCAAAA	ATTTTCANA	TGGTAGCTTT	CANATGTNCC	CTCAGTCCC	300
ATGTTGCTCA	GATAAATAAA	TCTCGTGAGA	ACTTACACC	CACCACAAGC	TTTCTGGGC	360
ATGCAACAGT	GTCTTTCTT	TNCTTTTTCT	TTTTTTTTT	TTACAGGCAC	AGAAAATCTCAT	420
CAATTTATT	TGGATAACAA	AGGGTCTCCA	AATTATATTG	AAAAATAAAAT	CCAAGTTAAC	480
ATCACTCTG	T					491

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA	GCAGGGCTAA	TTACCATAAG	ATGCTATTAA	TTAANAGGTN	TATGATCTGA	60
GTATTAACAG	TTGCTGAAGT	TTGGTATTTT	TATGCAGCAT	TTTCTTTTTG	CTTTGATAAC	120
ACTACAGAAC	CCTTAAGGAC	ACTGAAAATT	AGTAAGTAAA	GTTCAGAAC	ATTAGCTGCT	180
CAATCAAATC	TCTACATAAC	ACTATAGTA	TTAAAACGTT	AAAAAAAAGT	TTTGAAATCT	240
GCACACTGAT	ANACCGCTCC	TGTCAGGATA	ANACTGCTTT	GGAACAGAAA	GGGAAAANC	300
AGCTTTGANT	TTCTTTGTGC	TGATANGAGG	AAAGGCTGAA	TTACCTTGTG	GCCTCTCCCT	360
AATGATTGGC	AGGTCTNGGT	AATNCAAAAA	CATATTCCAA	CTCAACACTT	CTTTTCCNCG	420
TANCTTGANT	CTGTGTATTC	CAGGANCAGG	CGGATGGAAT	GGGCCAGCCC	NCGGATGTT	480
CANT						484

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAACACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCCT CTCAAGTGCC TTTTTGTTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCAGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAAC TGT	133

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCG CGTGTTCGCG TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GTAGGCT	147

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTC CTGTATACTC	60
TGATTACATA CATTATCCT TTAAAAAAAGA TGAAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TAACTAGTT	180
TTGACTTCTA AGTTGGT	198

## (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTC	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATACT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCCTCTTT ATTGGACTTC TTTGAAGAGT	330

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 175 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCTGGAACC ACCGGTGGCT GGGCAAGCCC CAGGAGTGC CG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACATT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAAGCACCTT TTGGCTTTCA AAACATGACCA TTTTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG CTCCCTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TGGTCTATAA NATGAAATCC CAANGGGAC AGAGGTCACT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AACACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGCGGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACCCCTTTCC CTCAGAATTC AGGAAAGAGA CTGTCGCCGT CCTCCTCCG TTGTTGCCTG	60
AGAACCCGTG TGCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCTGG TCTCTCTCCC AGTCCCCAGT TCACCUCTCCA TCCCTCACCT	180
TCCCTCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 385 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTCTCC CAGCACTTTA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTAAA AAAGGGACT TGCTAAAAAA AGAAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG	240
CTGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCCAG GGCCCCAGCC TG GCCACACC TGCTTACAGG GC ACTCTCAG ATGCCATAC	360
CATAGTTCT GTGCTAGTGG ACCGT	385

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTTAA TGG	73

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTC TTGGGGCCTC TCACCCCTCCT CTCCTGCAGC	60
TCCAGCTTTG TGCTCTGCCT CTGAGGGAGAC CATGGCGCAG CATCTGAGTA CCTCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGAGGCC AAGGAGGAGG ATAGGATAAT	180
CGCGSGTGGC ATCTATAACG CAGACCTAA TGATGAGTGG GTACAGCGTG CCCTTCACTT	240
CGCCCATCAGC GAGTATAACA AGGECACCAA AGATGACTAC TACAGACGTC CGCTGCGGGT	300
ACTAAGAGCC AGGCACACAGA CGTTGGGGG CCTGAATTAC TPCCTCGACG TAGAGGTGGC	360
CGGAACCATA TGTACCAAGT CGCAGCCAA CTGGACACCC TGTGCTTTCG ATGAAAGCC	420
AGAACTGCAAG AAGAAACAGT TGTGCTCTTT CGAGATCTAC GAAGTTCCCT GGGGAGAAC	480
GAANGTCCCT GGGTGAAATC CAGCTCTCAA GAAATCTAN GGATCTGTTG CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGGCCC TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAA CACGAGAAAG CACATACCA AA GGCACCCACA CACCACCTGT	180
CCAAAAGGC CTTCGATACTG GGATAATCCT ATTATATTAC TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTT CTGAGGCTTT TACCACTCCA GCCTAGCCCC TACCCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCCGCTAA ATCCCCCTAGA AGTCCCCACTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATT TACTGGGTCT CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAAAACACA TTTTCTACAT AGATAAGTACT	60
AGGTATTAAT AGATATGTAA AGAAAAGAAAT CACACCATTA ATAATGGTAA GATTGCTTTA	120
TGTGATTTA GTGGTATTTT TGGCAACCTT ATATATGTTT TCCAAACTTT CAGCAGTGT	180
ATTATTTCCA TAACTAAAAA AGTGAGTTTG AAAAGAAA TCTCCAGCAA GCTATCTCATT	240
TAAATAAAGG TTTGTCTCT TTAAAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA	360
AGTCAGTTTG CCTTGAAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAAATG	420
CTTCGTAATT TTGGAGTANG AGGTCCCTC CTCAATTTCG TATTTTAAAGTACATGS	480

TAAAAAAAAAA AATTCAACAAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC

533

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 511 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAAGAACAC	TAAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGGTTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCTT	GTCTGTTATG	420
ATTCTCTCC	ATTGAGCNA	AAAACCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTGAAG	NACCNGGAGG	A			511

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAG	TGGCAGCTCT	GGTGCCTGTG	TTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	TTAATCCTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240
CTCAGAAACC	TACTCAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	300
CTCTGCATTA	AATCTATTTG	CACTTCTGA	AAAAAAA	AAAAAAAGGG	CGGCCGCTCG	360
ANTCTAGAGG	GCCCGTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCTTCT	ANTTGCAGC	420
CATCTGTGT	TTGCCCTCTCC	CCCGNTGCC	TCCTTGACCC	TGGAAAGTGC	CACTCCCACT	480
GTCCTTCTCT	AANTAAAAT					499

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATT	GGATTCA	GGCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAGTAATAAG	GTAAAAGCTA	GTCTCTAACT	120
TCCAGGCCA	GGGCTCAAGT	GAATTTGAAT	ACTGCATT	CAGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGTG	TCCTACCACT	CTAACATCAA	240
AAAGAATIAC	AGACTCTGAT	ICTAAGTGA	TGATTGAATT	CTAAAAATGG	TAATCATTAG	300
GGCTTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTGCTT	GATATATTG	TTGATAATTAA	GATTCTGAC	TTATATT	AATGGGTTCT	420
ACTGAAAAN	GAATGATATA	TTCTTGAGA	CATCGATATA	CATTATT	CACTCTTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATCCC	CAAATTGTAT	GGTGATAAAA	GTCGGT	537

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO 75:

CAAAANACAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCCT	CAAGTAGTGT	GGTCTATTTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTTCT	GCTGCAANGG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAAG	AGGCCATCTT	TTCCTCATCG	GTTATTCTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTTCT	GGGTTTGGGC	CATTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACCNGT	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCAAATAGC	CGCTGCTATN	GTGTAGAAC	TCCCTGN		467

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGCC	GAGATCTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGG	GTACTCCAAA	GATTCAAGGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTCTC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAAAGTG	GAGCATTTCAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTTCT	ATCTCTTGTA	CTACACTGAA	TTCACCCCCA	300
CTGAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT 400

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 248 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CCGCGGGGG A TGCGAGGCTC GGAGCACCT TGCCCGGCTG TGATTGCTGC	120
CAGGCACTGT TCATCTCAGC TTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA	180
GTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA	240
AAAAAAAAA	248

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACAA	60
TCACCCAGAC CCCGCCCTGC CGCTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT	180
GATTTAAAAA AAAAAAAAAA A	201

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 552 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT CCTAGTAATT TCCTCGTAAT GATTCTGTAA TTACTTCCT ATTCTTTATT	120
CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAAATAC AAAAAGGTAG	180

TGTGATAGTA TAAAGTATCTA AGTGGCAGATG AAAGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACCT AAATTACTTT AATATGCTGT TGAAACCTACT	300
CTGTTCCCTTC GCTAAGAAAAA TTATATAAACCA GCACCTTGTT AGTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAAAA CTTGGGCTAT ACATAAANTA TAAAGAAATA CGGAATTAA	420
TTCCCAGGAA TATGCGGGTTC ATTATGAAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTTGGT TAATACGTTA ATATGCTCTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAAAAAA AA	552

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCCTCT TATTTTCAGA	60
GGGGAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTACAG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGATGATGTCC TTAGTCACTA	240
ACCTTAAACT TTCCCACCCA GAAAAGCCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300
TCTTCTAAAGT CCTCTTCCAG CCTCACTTIG AGTCCTCCTT GGGGGTIGAT AGGAANTNTC	360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAAAA AAAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGGCGCT TTCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAGC AGAACGCTAAA	GCCAAAGCCC AAGAACAGTG	GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT	GCCAGTGCCA GTGCCAGCAC	CAGTGGTGGC TTCAAGTGCTG	120
GTGCCAGCCT GACCAGCACT	CTCACATTTG GGCTCTTCGC	TGGCCTTGGT GGAGCTGGTG	180
CCAGCAGCAG TGGCAGCTCT	GGTGCCTGTC GTTTCTCCTA	CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTC	TCTTCAAGCC AGGGTGATC	CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA	TCAATCAATT GAAGTTGACA	CTCTGCATTA AATCTATTG	360
CCATTTCAAA	AAAAAAAAAAA AAA		383

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA	TCATGTCCTC CAGTATTACC	TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT	TGACCCGATG GGACAACAGA	CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA	ATACTCTCGA CACCGAATCA	CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC	GCGCCCTGTC CTCTGAGGGT	CCTTAAACTG	240
ATGTCTTTC TGCCACCTGT TACCCCTCGG	AGACTCCGTA ACCAAACTCT	TCGGACTGTG	300
AGCCCTGATG CCTTTTGCC AGCCATACTC	TTTGGCNTCC AGTCTCTCGT	GGCGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT	CACCCATNAA GGGAACACAT	TTGANNTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA	NTTCAGAATA AATGAATTGA	AAAAACTCTTA	480
ACCAACACAT		AAAAAAA AAAA	494

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANCC	CCTCCTGACCC CACGGGACAG	TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC	TACCTGAGA TCTTCGGGCA	GAATCCCCAG	120
GAGGACATGG ACAGTGGCCCT CATGGAGCAC	AGCAACTGCT CGTCGGAGCC	CGGCTTCTGG	180
CCACACCCCTC CTGGGGCCCA	GGCGGGCACC TGCGTCTCCC	AGTATGCCAA CTGGCTGGT	240
GTGCTGCTCC TCGTCATCTT	CCTGCTCGTG GCCAACATCC	TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC	GGCAAAGTAC AGGGCAACAG	CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG			380

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCTCTTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCACCA	CCTCTGCAT	CTTGCGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CGTCNATNA	AACTGTGGC	TGGTTGTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAG	GAGTGTGCA	TCTTCCCCAC	ACTTTTGATG	ACTTTATTGA	240
GTCGATTCTG	CATGTCAGC	AGGAGGTTGT	ACCAAGCTCTC	TGACAGTGAG	GTCACCAGCC	300
CTATCATGCC	NTTGAACGTG	CCGAAGAACAA	CCGAGCCTTG	TGTGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAAGA	NAGCCGTGGC	AAAAGANATT	GACAACTCGC	CCAGGNNGAA	420
AAAGAACACC	TCCTGGAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNNGC	GCNTNCCTT	480
T						481

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGCTG	AGAATTCA	60
ACTTGGAAAA	GCAACTTNA	GCCTGGACAC	TGGTATTAAA	ATTCCACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTGC	TCCCTTACTT	TGTCATCACC	AGTCTGGAA	TAAGGGTATG	180
CCCTATTCA	ACCTGTTAAA	AGGGCCCTAA	GCATTTTGA	TTCAACATCT	TTTTTTTGA	240
CACAAGTCCG	AAAAAAAGCAA	AAGTAAACAG	TTNTTAATT	GTTAGCCAAT	TCACITTTCTT	300
CATGGGACAG	AGCCATTG	TTTAAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAAGANTAG	CCTTTCTACT	TCACCAGACA	CAACTCCTT	CATATTGGGA	420
TGTTNACNA	AGTTATGTCT	CTTACAGATG	GGATGCTTT	GTGGCAATTC	TG	472

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAAACCA	GT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGCG	CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTAAAGCTTATG	120
CCTCTTGGT	ATCTATATCT GTGAAAGTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTCTG	TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTGAC	ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG	AAAAGCANAA CTGAACATNA GAAACAAATTN CCTGGTGAGA AATTNCATAA	360
ACAGAAATTG	GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTTT TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT	CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCGC	60
GTCCTAGCCN	ACCATGGCCG GGCCCCCTGGC CGCCCCGCTG CTCCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG	GCCGTGAGCC CCGCGGGCGG CTCCAGTCCC GCGAAGCCGC CGCGCCTGGT	180
GGGAGGCCA	TGGACCCCAGC GTGGAAGAAG AAGGTGTGCG GCGTGCCTG GACTTTGCCG	240
TCGGCNANTA	CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANAAA	TTGTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAAGAA	CCNAGCCAAT TNGAACAAATT NCCCCTCCAT AACAGCCCT TTTAAAAAGG	420
GAANCANTCC	TGNTCTTTTC CAAATT	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTTGTG	CACTGGCCAC TGTGATGGAA CCATTGGGG AGGATGCTTT GAGTTTATCA	60
GTAGTGATTC	TGCCAAAGTT GGTGTTGTA CATGAGTAG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG	GTCTGCATAT CAGCAGACAG TTTGTCGCTG TATTTTGTAG CTTTGAAGTT	180
CTCAGTGACA	AGTTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTGTAG CTTTGCATC	240
TTTNATGTTN	AGACTTGCCT CTNTNAAATT GCTTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAAA	TAGAANNACT TCTCTGCTTN GAANATTGAA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC	CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAAAANG GNTCCITCENN	420
AATTCNNANA	ANTTCAGNTN TCATACAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGCTGTAA	GCNTNTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCA	GCACATCTTC	TAGGACCTTT	TTGGATTCA	TTAGTATAAG	CTCTTCCACT	180
TCTTTGTTA	AGACATTCATC	TGGTAAAGTC	TAAAGTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTTGGCTGA	ACAACCCACC	TNAAGTCCT	300
TTGTGCATCC	ATTTAAATA	TACTTAATAG	GGCATGGTN	CACTAGGTTA	AATTCTGCAA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGCTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCTCTTT	GACTACCGTG	TGCCAGTGCT	GCTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACITG	NCTGGAACTA	GCAAGACATC	ACITACAAAT	TOACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCCAGT	300
TGTCAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTGTT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGCTT	CCCATTTCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCCACAAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCC	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCCT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACCTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGC3	GTCCACCAGG	ATGCCCCACT	GTGCGGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGUCCAGG	GUUUTTGUCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TGGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGGCCG	ACCTCACCGA	TGCCCANTGT	GTCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTG	CAGGTCAATG	TCGGTGAANC	CTCCGCGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCCGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAAGC	CTGCCTCTGG	CCTTCCCCCTC	120
CGCCTCAATG	CAGAACCA	AGTGGGAGCA	CTGTGTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTCC	CAATGCTAAT	TTCAAACAA	240
CAACAACAAA	ATAACATGTT	TGCCTGTTNA	GTTGTATAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTIACA	TATACTGCTT	GCAANTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAA					377

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG	GGTTAGGGTC	CAGTTCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGACCTGANG	CAGATTTCCC	ACAGTGACCC	CAGGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGGCCCA	TTCCGGGGCT	CTTCCCCGAG	GAGGAAGGG	AGGGGCTCTG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCCACACAAA	300
TGCAAGCTCA	CCAAGGTCCC	CTCTCAGTCC	CTTCCCTACA	CCCTGAACGG	NCACTGGCCC	360
ACACCCACCC	AGANCANCCA	CCCGCCATGG	GGAATGTNCT	CAAGGAATCG	CNGGGCAACG	420
TGGACTCTNG	TCCCNNAAAGG	GGGCAGAATC	TCCAATAGAN	GGANNGAAC	CTTGCTNANA	480
AAAAAAAANA	AAAAAA					495

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCAG	AGCGGACTTT	GTAATTGTTG	GAGAAATACT	GCTGAATTT	120
TAGCTGTTT	GAGTGATTC	GCACCACTGC	ACCACAACTC	AATATGAAAAA	CTATTTNACT	180
TATTTATTAT	CTTGTGAAAAA	GTATACAATG	AAAATTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGAAAAA	TGTGGAGTGT	ATGTTCTTT	CACAGTAATA	TATGCCTTTT	GTAACCTCAC	360
TTGGTTATTT	TATTGTAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTCTTT	CTTGTGTTAC	CTTAATTITC	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 475 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAAC	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTGGTGAAT	TTCAAAATTA	TATGTAACCT	CTACTAGTTT	TACTTTCTCC	CCCAAGTCTT	120
TTTTAACTCA	TGATTTTAC	ACACACAATC	CAGAACATTAT	TATATAGCCT	CTAAGTCTTT	180
ATTCTTCACA	GTAGATGATG	AAAGAGTCT	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAAT	300
TGTGTTAGTC	TCAATTCTCA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTCTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTCTA	ATGCTGATAT	GATCTTGAGT	ATAAGAATGC	ATATGTCACT	AGAATGGATA	60
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AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGAAA TCAAAACTCA CAAGTGCTCA TCTGTTGAG ATTGTGTTGA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTTCT CANATCTTGG CCAATNTTCC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AATTTTTAA NAATACACTT	300
GTGATTATNA ATTAATCAC AAATTTCACT TATAACCTGCT ATCAGCAGCT AGAAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCAC TGACA ATCAGACCTA	60
TGCTAGTTCC TGTCA TCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAAG TTTCCCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACAA GAGAAATAAA OTCAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGCTGTATCC TGGTGC CGTCTTATGAA CTGACCACCC	420
TTTGGAAATAA TCTTGACGCT CCTGAACCTTG CTCCCTCTGCG A	461

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGGTGTGTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCGTCCT	60
CGGCGCCTCT CGGGGCCCGA GGAGGAGCGG CTGGCGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTCTCT AGCGATCTGA GAGGC GTGCC TTGGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (v) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TCCAACCTCCA GCTGGGGCCG TGCGGACGAA	SATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGC GCGACAGTCG CAGGTGCAGC	CGGGGCGCCCT GGGGTCTTGC	120
AAGGCTGAGC TCACCCCCCA GAGGTCGTCT CACGTCCCAC	CACCTTGACG CCSTCGGGCA	180
CAGCGGGAAC AGAGCCCCGGT GAAGCGGGAG	GCCTCGGGGA CGCGCTUGGG AAGGGCGGCC	240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC		269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGGAAATC TACTGCGAGC ACAGCAGGTC	AGCAACAAGT TTATTTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCA	GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG	AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT	GGGGCAGTTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG	GATATCTTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GTTTCTTGC CAAATCCAAC	AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATATTTC TCATATCGGT	GGCCA	405

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	TTTTTTTTTT	60
GGCACCTTAAT CCATTTTTAT TTCAAAATGT CTACAAATTT	AATCCCATT ACGGTATTT	120
TCAAATCTA ATTATTCAA ATTAGCCAA TCCTTACCAA	ATAATACCCA AAAATCAAAA	180
ATATACTTCT TTCAGCAAAC TTGTTACATA AATTAAAAAA	ATATATACGG CTGGTGTGTT	240
CAAAGTACAA TTATCTTAAC ACTGCAAACA TTTTAAGGAA	CTAAAATAAA AAAAAACACT	300
CCGCAAAGGT TAAAGGAAC AACAAATTCT TTTACAACAC	CATTATAAAA ATCATATCTC	360
AAATCTTAGG GGAATATATA CTTCACACGG GATCTTAAC	TTTACTCACT TTGTTATTT	420
TTTTAAACCA TTGTTGGC CCAACACAAT GGAATCCCCC	CTGGACTAGT	470

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTT	TTTTTTTGA	CCCCCTCTT	ATAAAAACA	AGT TAC CATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAAATGGAAA	CTGCCTTAGA	TACATAATTG	TTAGGAATTG	GCTTAAAATC	TGCCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAACAC	ATCCAAATTG	240
ATTTTTCTTG	TCTTAAAT	TATCTAATCT	TTCCATTTT	TCCCTATTCC	AAGTCAATTG	300
GCTTCTCTAG	CCTCATITCC	TAGCTCTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAA	360
AGGGAAAACA	CGAACAGAGAA	TGGCACACAA	AACAAACATT	TTATATTTCAT	ATTTCTACCT	420
ACGTTAATAA	AATAGCATTT	TGTGAAGCCA	GCTCAAAGA	AGGCTTAGAT	CCTTTTATGT	480
CCATTTTGT	CACTAAACGA	TATCAAAGTG	CCAGAACATG	AAAGGTTTGT	GAACATTAT	540
TCAAAAGCTA	ATATAAGATA	TTTCACACATAC	TCATCTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT	TTTTTCTCTT	CTTTTTTTT	GAAATGAGGA	TCGAGTTTT	60
CACTCTCTAG	ATAGGGCATG	AAGAAAACTC	ATCTTCCAG	CTTAAAATA	120
CTCTTATGCT	ATATCATATT	TTAAGTTAA	CTAATGAGTC	ACTGGCTTAT	180
AGGAAATCTG	TTCATCTTTC	TCATTCTAT	AGTTATATCA	AGTACTACCT	240
GAGGTTTTTC	TTCTCTATTT	ACACATATAT	TTCCATGTGA	ATTGTATCA	300
TTCATGCAA	CTAGAAAATA	ATGTTTCTTT	TGCATAAGAG	AAGAGAACAA	360
CAAAACTGCT	CAAATGTTT	GTAAAGTTAT	CCATTATAAT	TAGTTGGCAG	420
AAATCACATT	TACGACAGCA	ATAATAAAAC	TGAAGTACCA	GAGCTAATAC	480
AAAGGAACAT	TTTTAGCCTG	GGTATAATTG	GCTAATTAC	TTTACAAGCA	540
TGAATTACA	TGTTATTATT	CCTAGCCCAA	CACAATGG		578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTGTGATG	TTCAGTA	ATAATCAGAA	CAATATTAA	TTTATATTT	AAAATTCTATA	60
GAAAAGTGC	TTACATTAA	TTAAAGTTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTAA	TTTGAGGAAA	ATACACCCAA	ATACATTAAG	TAAATTATTT	180
AAGATCATAG	AGCTGTAAAG	TGAAAAGATA	AAATTTGACC	TCAGAAACTC	TGAGCATCAA	240
AAATCCACTA	TTAGCAAATA	ATTACTATG	GACTTCTTGC	TTAAATTTC	TGATGAAATAT	300
GGGGTGTCA	TGGTAAACCA	ACACATTCTG	AAGGATAACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTCTTCAA	TCTTTTAAGG	420
GGCGAGAAAT	GAGGAAGAAA	AGAAAAGGAT	TACGCATACT	GTCTTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAAGAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	548

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT	TTTTTAGTC	AAGTTCTAT	TTTTATTATA	ATTAAGTCT	TGGTCATTTC	60
ATTTATTAGC	TCTGCAACTT	ACATATTAA	ATTAAGAAA	CGTTTAGAC	AACTGTACAA	120
TTTATAATG	TAAGGTGCCA	TTATTGAGTA	ATATAATTCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGCAACATTA	TTTAATTTC	ATTAGTAGAT	ATACACTGCT	240
GCNACCCCTA	ATTCTCTCT	CCATCCCCAT	GTGATATTGT	GTATATGTG	GAGTTGGTAG	300
AATGCATCA	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCGCTG	CCACATTGTC	GGCTCTTGC	ACTTGTTC	AAA	473

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGGCA	TCTCGGTCA	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCCGTT	60
CTGTGCTATG	GTCCTGGCTG	ACTTCGGGGC	CGGTGTGGTA	CGCGTGGACC	GGCCCGGGCTC	120
CGCGTACGAC	GTGAGTCGCT	TGGCGGGGG	CAACCGCTCC	CTAGTGCTGG	ACCTGAAGCA	180
GGCGCGGGGA	GCCGCGGTGC	TGCGGCGTCT	GTGCAAGCGG	TCGGATGTGC	TGCTGGAGCC	240
CTTCGGCGCG	GGTGTATGG	AGAAACTCCA	GCTGGGCCA	GAGATTCTGC	AGCGGGAAAAA	300
TCCAAGGCTT	ATTTATGCCA	GGCTGAGTGG	ATTTGCCAG	TCAGGAAGCT	TCTGGGGTT	360
AGCTGGCAC	GATATCACT	ATTTGGCTTT	GTCAGGTGTT	CTCTAAAAAA	TTGGCAGAAC	420
TGCTGAGAAT	CCGTATGCC	C3CTGAATCT	CCTGGCTGAC	TTTGCTGGTC	CTGGCCTTAT	480
GTGTGCACTG	GGCATTATAA	TGGCTCTTTT	TGACCGCACA	CGCACTGACA	AGGGTCAGGT	540

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA	600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT	660
CTATACGACT TACAGGACAG CAGATGGCA ATTATGCCCT CTTGCACCAA TAGAACCCCA	720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTT CCAATCAGAT	780
GAGCATGGAT GATTGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAAGAC	840
GAAGGCAGAG TGCTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC	900
TTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA	960
CGACCCAGGAC GTCACCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCCAG CCATCCCTTC	1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAAG AATTGGATT	1080
CAGCCGCGAA GAGATTTATC AGCTTAACCTC AGATAAAAATC ATTGAAAGTA ATAAGGTAAA	1140
AGCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG	1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTAA CAGTGTCTTA	1260
CCACTCTAAT CAAGAAAAAGA ATTACAGACT CTGATTTAC AGTGTGATT GAATTCTAAA	1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACTTGGG TACTTATACT AAATATGGT	1380
AGTTATTCTG CCTTCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTC TTGACTTATA	1440
TTTGAAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT	1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGT	1560
AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1620
A	1621

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 382 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

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Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195         200         205

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Glu Gln Asn Met Leu Asp Glu Gly Ala Pro Phe Tyr Thr Thr Tyr Arg  
 210 215 220  
 Thr Ala Asp Glu Glu Phe Met Ala Val Glu Ala Ile Glu Pro Glu Phe  
 225 230 235 240  
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro  
 245 250 255  
 Asn Gln Met Ser Met Asp Asp Trp Phe Glu Met Lys Lys Lys Phe Ala  
 260 265 270  
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp  
 275 280 285  
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val  
 290 295 300  
 His His Asp His Asn Lys Glu Arg Gly Ser Ile Thr Ser Glu Glu  
 305 310 315 320  
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala  
 325 330 335  
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu  
 340 345 350  
 Ile Leu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn  
 355 360 365  
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO 109

- (i) SEQUENCE CHARACTERISTICS.
- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM Homo sapiens

(xi) SEQUENCE DESCRIPTION. SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGGGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCTGGCC	ATGCCTCACT	GAGCCAGCGC	CTGCGCTCT	ACCTGCCGA	CAGCTGGAAC	120
CAGTGCAGCC	TAGTGGCTCT	CACCTGCTTC	CTCCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGTACC	ACCTGGGCCG	CACTGTCCTC	TGCATGACT	TCATGGTTTT	CACGGTCCCC	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CCTGASCAAC	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTGGCG	TGTGGCTGGT	AGCTATGGC	360
GTGGCCACGG	AGGGCTCCT	GAGGCCACGG	GACAGTGA	TGCCAAGTAT	CCTGOSCCG	420
GTCTTCTACC	GTCCCTACCT	GCAGATCTTC	GGGCAGATTG	CCCAGGAGGA	CATGGACGTG	480
GCCCCTCATGG	AGCACAGCAA	CTGCTCGTGT	GAGCCCGGCT	TCTGGGCACA	CTTCTCTGGG	540
GCCCAGGCCG	GCACCTGCGT	CTCCCACTAT	GCCAACCTGGC	TGGTGGTGCT	GCTCCCTCGTC	600
ATCTTCTGTC	TCGTGCCAA	CATCCCTGCTG	GTCAACTTSC	TCATTGCCAT	GTTCAGTTAC	660
ACATTCCGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTTGA	AGGGCAGCG	TTACCGCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCAGCGTGT	GGCCCGCCCT	TATCGTCAT	CTGCCACTTG	780
GGCCTCTGTC	TCAGGCAATT	GTGCAGGCCG	CCCGGGAGCC	CCCAGCCGTC	CTCCCGGGCC	840
CTCGAGCATT	TCCGGGTTTA	CTTTCTAAG	GAAGCCGAGC	GGAAAGCTGCT	AAAGTGGGAA	900
TCCGGTGCATA	AGGAGAACTT	TCTGCTGCCA	CGCGCTAGGG	ACAAGGGGA	GAGCGACTCC	960
GGCGCTCTGA	AGCGCACGTC	CCAGAACGTC	GACTTGGCAT	TGAAACAGCT	GGGACACATC	1020
GGCGAGTAGC	AAACAGCGCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCGGGGTC	1080
CTGGGGTGCG	TGGCGGAGGC	CCTGAGCGCG	TCTGCCCTG	TGCCCGCAGG	TGGGCGGCCA	1140
CCCGCTGACG	TGCCTGGGTC	CAAAGACTGA	GGCGTGTG	GGGAGTTGAA	GGAGAAAGCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGC	CTCGGCCCCC	GCACCTGGTG	1260
GGCTTGTCTT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TCTCAGGACC	ACCTTTGCCA	1320
GTGTCACTCT	TACAAACCAC	AGCATGCCG	GTCTCTCCA	GAACCAAGTCC	CAGCTGGGA	1380

GGATCAAGGC CTGGATCCCG GGCGTTATC CATCTGGAGG CTGCAGGGTC CTTGGGTAA	1440
CAGGGACAC AGACCCCTCA CCACTCACAG ATTCCCTACA CTGGGAAAT AAAGCCATT	1500
CAGAGGAAAA AAAAAAAA AAAA	1524

## (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3410 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.110:

GGGAACCAGC CTGCACGCGC TGGCTCCGGG TGACAGCCGC GCGCCTCGGC CAGGATCTGA	60
GTGATGAGAC GTGTCCCCAC TGAGGTGCC CACACCGAGCA GGTGTTGAGC ATGGGCTGAG	120
AAGCTGGACC GGCACCAAAG GGCTGGCAGA AATGGGCGCC TGGCTGATTC CTAGGCAGTT	180
GGCGGCAGCA AGGAGGAGAG GCCGCAGCTT CTGGAGCAGA GCGAGACGA AGCAGTTCTG	240
GAGTGCCCTGA ACGGCCCCCT GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG	300
GGTGAGCCGC CTGCTGCCGC ACCGAAAGC CCAGCTCTTG CTGGTCAACC TGCTAACCTT	360
TGGCCTGGAG GTGTGTTGG CCGCAGGCAT CACCTATGTG CGGCCCTCTGC TGCTGGAAGT	420
GGGGTAGAG GAGAAAGTCA TGACCATGGT GCTGGGCATT CGTCCAGTGC TGGGCCTGGT	480
CTGTGTCCCG CTCCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCCGCCGCCG	540
GCCCTTCATC TGGGCACTGT CCTTGGGCAT CTCGGTGAAGC CTCTTCTCA TCCAAGGGC	600
CGGCTGGCTA GCAGGGCTGC TGTGCCCCGA TCCCAGGCC CGGAGCTGG CACTGCTCAT	660
CCTGGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTG TTCACCTCCAC TGAGGCCCCT	720
GCTCTCTGAC CTCTTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCCTT	780
CATGATCAGT CTTGGGGCT GCCTGGGCTA CCTCTGCCTC GCCATTGACT GGGACACCAAG	840
TGCCCTGGCC CCCTACCTGG GCACCCAGGA GGAGTGCCTC TTGGCCTGC TCACCCCTCAT	900
CTTCCTCACC TGCGTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAGCGC TGAGGCCAC	960
CGAGCCAGCA GAAGGGCTGT CGGCCCTCTC CTTGTGCCCG CACTGCTGTC CATGCCGGGC	1020
CCGCTTGGCT TTCCGGAACC TGGGCGCCCT GCTTCCCCCG CTGCACCCAGC TGTCGTGCCG	1080
CATGCCCGC ACCCTGCCGC GGCTCTCGT GGCTGAGCTG TGCACTGGA TGCACTCAT	1140
GACCTTCACG CTGTTTACA CGGATTCCTGT GGGCGAGGGG CTGTACCAAGG CGGTGCCAG	1200
AGCTGAGCCG GGCACCGAGG CCCGGAGACA CTATGATGAA GCGGTTCGGA TGGCAGCCT	1260
GGGGCTGTTC CTGCAGTGC CGCATCTCCCT GGTCTTCTCT CTGGTCATGG ACCGGCTGGT	1320
GCAGCGATTC GGCACCTCGAG CAGTCTATTT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC	1380
CGGTGCCACA TGCCTGCTCC ACAGTGTGGC CGTGGTACA GCTTCAGCG CCCTCACCGG	1440
GTTCACCTTC TCAGCCCTGC AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGG	1500
GAAGCAGGTG TTCCCTGCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG	1560
CCTGATGACC AGCTTCTGC CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACAGT	1620
GGGTGCTGGA GGCAGTGGCC TGTCTCCACC TCCACCGGG CGTCTGCCGGG CCTCTGCCCTG	1680
TGATGTCCTCC GTACGTGTGG TGGTGGGTGA GCGGACCGAG CGCAGGGTGG TTCCGGGCCG	1740
GGGCATCTGC CTGGACCTCG CCATCTGGG TAGTGCCTTC CTGCTGCTCC AGGTGGCCCC	1800
ATCCCTGTTT ATGGGCTCCA TTGTCAGCT CAGCCACTCT CTCACTGCCCT ATATGGTGTG	1860
TGCCGCAGGC TGCGCTCTGG TCGCCATTAA CTTGCTACA CAGGTAGTAT TTGACAAGAG	1920
CGACTTGGCC AAATACTCAG CGTAGAAAAC TTCCAGCACA TTGGGCTGGA GGGCTGCCCT	1980
CACTGGGTCC CAGCTCCCCG CTCCCTGTAG CCGCATGGG CTGCGGGCT GGGCGCCAGT	2040
TTCTGTTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGTGCTGCT GAGGTGGGTA	2100
GCTGCACAGC TGGGGCTGG GGCCTCCCTC TCCCTCTCTCC CGAGTCTCTA GGGCTCCCTG	2160
ACTGGAGGCC TTCCAAGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCC GAAGGGCTCC	2220
ATGCACTGGA ATGCGGGGAC TCTGCAGGTG GATTACCCAG GCTCAGGGTT AACAGCTAGC	2280
CTCCTAGTTG AGACACACCT AGAGAAGGGT TTTGGGAGC TGAATAAACT CAGTCACCTG	2340
GTTCCTCCATC TCTAAGCCCC TTAACCTGCA GCTTCGTTA ATGTAGCTCT TGCAATGGGAG	2400
TTTCTAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTG TAGGGGAAGA	2460
GTCCTGAGGG GCAACACACCA AGAACCAAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT	2520

GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTGCCCATCA	2560
CAGAGACACA GGCATTTAAA TATTAACTT ATTTATTTAA CAAAGTAGAA GGAAATCCAT	2640
TCTAGCTTT TCTCTCTTGC TCTCTAATAT TTGGCTAGGC TGGGCGATCC CCNACAAATCA	2700
GGTCCTCTUA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATUTTCTT CTCTCTGGGT	2760
CTGGCCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC TACTCATCCC AAATGATAAT	2820
TCCAATGCT GTTACCCAAG GTTACGGGTG TGAGGAAGG TAGAGGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTTCCC CCCACTTCCA	2940
CTCCCTCTTA CTCTCTTAG GACTGGGCTG ATGAAGGCAC TGGCCAAAAT TTCCCTCTACC	3000
CCCAACTTTC CCTACCCCCC AACTTCTCCC ACCAGCTCCA CAACCTCTTGT TGAGCTACT	3060
GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTGT TCCATCTAG CCCCTAGAGT	3120
ATATCTGTGC TTGGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGGTTTAAGT GCCGTTGCA ATAATGTCGT CTTATTTATT	3240
TACCGGGCTG AATATTTAT ACTGTAAGTG AGCAATCAGA CTATAATGTT TATGCTGACA	3300
AAATTAAAGG CTTTCTTATA TGTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3360
AAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCCTTT	60
GTGGAGCCTC AGCAGTTCCC TCTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA	120
CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTTC	180
TGTGTGGTGC AGCCCTGTTG GCAGTGGGCA TCTGGGTGTC AATCGATGGG GCATCCTTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCGCAGC CGGCCTGTG GTCTTGCTC TTGGTTCTT GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCCTCATC TTCATTGCTG	420
AGGTTGCAGC TGCTGTGGTC GCCTTGGTGT ACACCACAAT GGCTGAGCAC TTCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACCAC CATGAAAGGG CTCAAGTGC GTGGCTTCAC CAACATACG GATTTTGAGG	600
ACTCACCCATA CTTCAAAGAG AACAGTGCCT TTCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGCAACCAAGC AAAAGGCTCA CGACCAAAAAA GTAGAGGGTT	720
GCTTCAATCA GCTTTGTAT GACATCCGAA CTAATGCAGT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACCTCTGC CTCTGCCACT ACTGCTGCCA CATGGAACT GTGAAGAGGC	900
ACCCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA	960
GAATGGACCT GCCCCTTCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CTTTTTAGCG	1020
ATGCCTGACT TTCCCTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCCA TTCCCCAGT CTATTAACCC CTTGATATGC CCCCTAGGCC	1140
TAGTGGTGTGAT CCCAGTGCCT TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT	1200
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACCC	1260
TGTTACAATG TTAAAAAAA AAAAAAAAAA	1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln  
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe  
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Tyr Leu Val Ala Tyr Gly Val Ala  
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu  
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro  
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser  
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys  
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe  
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe  
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln  
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr  
210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 553 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly  
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
 225 230 235 240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
 245 250 255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
 260 265 270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
 275 280 285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gin Gly Val  
 290 295 300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305 310 315 320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
 325 330 335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
 340 345 350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
 355 360 365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
 370 375 380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385 390 395 400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
 405 410 415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
 420 425 430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
 435 440 445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
 450 455 460  
 Ala Cys Asp Val Ser Val Arg Val Val Gly Glu Pro Thr Glu Ala  
 465 470 475 480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
 485 490 495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
 500 505 510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
 515 520 525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530	535	540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala		
545	550	
(2) INFORMATION FOR SEQ ID NO:114:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 241 amino acids		
(B) TYPE: amino acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: protein		
(vi) ORIGINAL SOURCE:		
(A) ORGANISM: Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:		
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu		
1	5	10
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val		
20	25	30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser		
35	40	45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly		
50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
80		
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
160		
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTTCTC TCCCCTCCTC TGAATTAAT TCTTTCAACT TGCAATTGCG AAGGATTACAGATGTATAT TGTGTTGCAA AAAAAAAA GTGCTTTGTG TAAAAATTAC	60 120 180 240 300 360 366
TTGGTTTGTG AATCCATCTT GCTTTTCCC CATTGGAACT AGTCATTAAC CCATCTCTGA ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT	
TCTCAGAACC ATTTCACCCA GACAGCCTGT TTCTATCCGT TTTAATAAT TAGTTGGGT TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTCACAT AAAAGTCTGT GACTTGAAAGTTAGTC	

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTCCT ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA AGACTTTACT ATTTTGTAT TTTAAGACAC ATGATTTATC CTATTTAGT AACCTGGTTC ATACGTTAAA CAAAGGATAA TGGAACAGC AGAGAGGATT TGTTGGCAGA AAATCTATGT TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	60 120 180 240 282
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(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAAG GATGTGGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGAA TCTCTGATTG CCGCACAAATC TGAGTGGAAA	60
AANTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACACACA	60
AAAAATGGGG TGAAATTGGC CAACTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAACG CGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCACAACATG CTGGGGTGGT	90

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANCAGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AACCTTGAA GTCATTTGAA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCTAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CAITTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAG	171

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCCTGA ACACACACAGA ATGGTGCGGCG TTGTGCTATC CAGCAACACA TTTATTATCA	60
TTATCAANTA TTGTGT	76

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTC ATTCTCTTGG	120
TTAACAGATTG T	131

## (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 432 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCCTG CATTGCGAG AAATGAAGAT GAATTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG	240
CTCTTGAACT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTCATC TCTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTTGCTT GT	432

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY linear

(ii) MOLECULE TYPE cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACTTC AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATT ATAAAAATT GT	112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTTTCTAA TGTCTCCCCT CTACCAAGCTC	60
ACCTGAGATA ACAGAACATGAA AATGGAAGGA CAGCCAGATT TCTCCCTTGCG TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGTTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT	240
TTCCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTTGTATC ACTCTGACTT TTTAGCATAAC	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTTCATC	120

TAGAACATTG ATCTTGATATA NAAAGATAAGG TGAGTTTATG TTCTTCACG TTGGCCATG	180
GATAAACAAA GT	192

## (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTCATGG TGTTTGCGG ATCTTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTC CATTTCGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTATTTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATGTGC AGCACTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

## (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA CCTGTAAAT CTGATGTGAT TTGCTTTATT ATCCAACCAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNNGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

## (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTCGGCACATT	CTCCTGAAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAACCTCGAT	TTCAAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTTG	TATCTCGGGT	180
TTTAGCAAGT	AAAAATGAAN	ATGACAGGAA	AGGCTTATT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAAC	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGAAAGCCT	300
GTAACAAATCT	ACAATTGGTC	CA				322

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTAT	CTGCATAATT	60
CTTGTCCCC	TTTCCATCTG	GCTCCTGGGT	TGACAATTG	TGGAAACAAC	TCTATTGCTA	120
CTATTTAAAA	AAAATCACAA	ATCTTTCCCT	TTAAGCTATG	TTNAATTCAA	ACTATTCCCTG	180
CTATTCCCTGT	TTTGTCAAAG	AAATTATATT	TTTCAAATA	TGTNTATTG	TTTGATGCCGT	240
CCCACGAAAC	ACTAATAAAA	ACCACAGAGA	CCAGCCTG			278

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GT TTANAAAAA	CTTGTAGC	TCCATAGAGG	AAAGAATGTT	AAACTTGT	TTTTAAAACA	60
TGATTCTCTG	AGGTAAACT	TGGTTTCAA	ATGTTATT	TACTTGTATT	TTGCTTTGG	120
T						121

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATTTAAAACC ATGCCCTAGCA CATCABAATC CCTCAAAGAA CATCAGTATA ATCTTATAAC	60
ATANCAAGTG GTGACTGGTT AAGGGTCCGA CAAAGGTAG CTGGCACATT ACTTGTGTGC	120
AAACTTGATA CTTTTGTTCT AAGTAGGAAC TAGTATACAG TNCCTAGGAN TGTTACTCCA	160
GGGTGCCCGG CAACTCCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACCTTCGCT	240
CCAACTCAAT CAAGCCCTGG CCCATCTAAC CTGGCAATTGG CTGAACAAAC GTTGCTGAG	300
TTCCTCAAGGA TGCAAAGCCT GGTGCTCAAC TCCCTGGGGCG TCAACTCAGT	350

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GGCCAGGGTT	60
GCTGTGATTG TATCCGAATA NTCCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT	120
GCAGACTTGT GTCTGCCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA CAAACNCCAAG	240
AAAACACTGCAG AGGCCCGAGG TCAGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC	300
TCCCAGGAAC CGGGCAGAAC GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT	399

## (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTC TGTGAACGTA GGGATGTAGA NGTTTGCCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCA TGGTGGGGTT CCTGT	165

## (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACCTTCTC CAGTAAGAAT CAGGGACTTG AATGGAAAC GTTAACAGCC ACATGCCAA	120
TGCTGGGAG TCTCCCATGC CTTCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAGAGTGC TTGGGGTGA GGGCTGGGG CATANANGGT	240
CANGCCTCAC GAAGCCTCAA GTTCCATTCA GCTTGCCAC TGTACATTCC CCATNTTTAA	300
AAAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAAATTTC	338

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCCGAA GTGAAGGAGA	120
ATTCAAAACAG ACCTCGTCAT TCCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180
ATTTGCCTTA CTCAGGGTGT ACCGGACTCT GGCCCCGTAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCTACCA CTGCTGAGTG	360
GCCTGGAACT TGTAAAGT GT	382

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAAANCTT CTTTCTGTTG TGTNGATTT TACTATAGGG GTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTAAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTS	120
TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATTTC	180
ATATTCAAGCA TAAAGGAGAA	200

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid

9.1

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (iii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT	CAAAACACTC	ATATGTTGCA	AAAAACACAT	AGAAAAAATAA	AGTTTGGTGG	60
GGGTGCTGAC	TAAACTCAA	GTCACAGACT	TTTATGTCAC	AGATGGAGC	AGGGTTTGT	120
ATCCATGTA	AGAACCCAAA	CTAATTATT	AAACACCATA	CAAACAGGCT	GTCTGGCTCA	180
AATGGTTCTG	AGAACCATCC	AATTCACTG	TCAGATGCTG	ATANACTAGC	TCTTCAGATG	240
TTTTTCTACC	AGTTCAGAGA	TNGGTTAATG	ACTANTCCA	ATGGGGAAAA	AGCAAGATGG	300
ATTCACAAAC	CAAGTAATT	AAACAAAGA	CACTT			335

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA	TATTGCCACA	TATATCCTTT	CCAATTGCCG	GCTAACACAGA	CCTGTATT	60
GGGTTGTTA	AAGACAACCC	AGCTTAATAT	CAAGAGAAAT	TGTGACCTTT	CATGGAGTAT	120
CTGATGGAGA	AAACACTGAG	TTTGACAAA	TCTTATT	TTCAAGATAGC	AGTCTGATCA	180
CACATGGTC	AAACACACTC	AAATAATAAA	TCAAATATNA	TCAGATGTTA	AAGATTGGTC	240
TTCAAAACATC	ATAGCCAATG	ATGCCCGCT	TGCCTATAAT	CTCTCCGACA	AAAAACCCACA	300
TCAACACCTC	AGTGGCCACC	AAACCATTCA	GCACAGCTTC	CTTAAGTGTG	AGCTGTTGGA	360
AGCTTACCACT	CTGAGCACTA	TTGACTATNT	TTTCANGCT	CTGAATAGCT	CTAGGGATCT	420
CAGCANGGGT	GGGAGGAACC	AGCTAACCT	TGGCGTANT			459

## (2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 140 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCCCT	CCACCAAAGTC	AGGACTCCTG	GCTTCTGTGG	GAGTTCTTAT	CACCTGAGGG	60
AAATCCAAAC	AGTCTCTCCT	AGAAAAGGAAT	AGTGTCAACCA	ACCCCACCCA	TCTCCCTGAG	120
ACCATCCGAC	TTCCCTGTGT					140

## (2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTCT	60
ATCTTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TAGAAATTTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTGTAAAT GGAAACATC CAGNAGCAAT TCCTAACCAA	60
ACTGGAGGGT ATTATACCC AATTATCCC TTCATTAACA TGCCCTCCTC CTCAGGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGTG ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCTTTGC CAACAGGCCT	120
CCTGAAGTCAGG GCTGGGATTG GTTCCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCCC CTGGCCTGTG CACACCTACT GATGACCTTC TGTCCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

## (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGSATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATAATGTA TATATIATTC AGTICQAIGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SCURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCT TATCTCATCG AATTTTTAAC CCAAACTCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTCGTCCCTAG TGGCCATCG TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCCTGCTC TCTAACCCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG ACCATTTAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCT	120

GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACAA	160
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGGG T	111

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAC	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCAC TGTTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCCTTT TCATCTAGTG GTGAAACCT GATGCTTAT GTTGACAGGA ATAGAACCAAG	120
GAGGGAGTTT GT	132

## (2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTGATGCC TCCAAACATG AAAGTGTCA	60
CTTCTGCTCT TATGTCTCA TCTGACAAC TTTTACCAT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCAC CCCCCCTCCT GGTGACCCC ATCTGTGAAG TCCTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCGGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACACCT AACTCCCCT GGCCCTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG	60
GAAAGTGCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGCCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240

GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGSCATCCTC	300
GCCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT	180
CTAATATATT CTCAATAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGCCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTGG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAAGT	120
GCCTGGGTAA TTCACCATTAA ATTTCCCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT	180

100

CTGGTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGUA TTTGGGATCC CAGTGAACTA	240
NATGTTGTGTA GCCTGCATA CTTAGCCCTT CCCACUCACCA AACGGAGTGS CAGACTGGTG	300
CGAACCCCTGT TTTCCCACTC CACCTABACA GATTACACATC CGGGAAATTCTC GAAACCTCGA	360
NACAGACGGG CTUTTTGCGAG AGCGGGGACT CTGAGANGGA CATGAGGGGU TCTGCUCTCGG	420
TGTTCATTTCT CTGATGTCCT GT	447

## (2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTTG	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACAGGCCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGGCGGCT GTGGTAGGTT GTGGGCTCTI CAACAGGGGC	240
TGCTGTGGTG CCGGGGAGNTG AANGTGTGTTG GTCACATTGAG CTGGGCCAGG TCTGGAAAGT	300
ANTANATTCT TCCCTGAGGC CAGCGCTTGTG GGAGCTGGCA NGGGTCANTG TTGTGTGTAA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCTN	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCGNGCTGTG GAAGGTTGTA NATTGTCACC	480
AAGGGAATAA GCTGTGGT	498

## (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACATCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCCTGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCACCC ACTCTGTGA AGAGATGCC CATGACCCCA GATGCCCTCTE	240
CCACCCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTE TGTATAATTG TAACATCCTG	300
GAGAAAAAATG GCAGTTGAC CGAACCTGTT CACAAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

## (2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGGCGTTGT CGTTCAAGGT GTATTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA	60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGGGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA	TGAATGTCT	CCTGGCCAGC	CTTGTGATCT	TTGCCACCTT	CGTGACTTTA	60
TCCAAATGCAT	CATGCTATTT	CATACTANT	CAGGGAGTTG	CAGGAGATTG	AACCAGGAAA	120
TGCAAGGATC	TCAAAGGAAA	CAAACAUCCA	ATAAACUUGG	AGTGGGAGAC	TGACAACGTG	180
GAGACATGCA	CTTGTGTACGA	AACAGAAAATT	TCATGTTGCA	CCCTTGTTC	TACACCTGTG	240
GGTTATGACA	AAGACAAC TG	CCAAAGAAATC	TTCAAGAAGG	AGGACTGCAA	GTATATCGTG	300
GTGGAGAAGA	AGGACCCAAA	AAAGACCTGT	TCTGTCAGTG	AATGGATAAT	CTAATGTGCT	360
TCTAGTAGGC	ACAGGGCTCC	CAGGCCAGGG	CTCATTCCTC	TCTGGCCTCT	AATAGTCAAT	420
GATTGTGTAG	CCATGCCAT	CAGTAAAAAG	ATNTTTGAGG	AAACACTTT		469

## (2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT	ATANATATCG	ACATTGCCGG	CACTTGTGTT	CAGTTTCATA	AAGCTGGTGG	60
ATCCGCTGTC	ATCCACTATT	CCTTGGCTAG	AGTAAAAAATT	ATTCTTATAG	CCCATGTCCC	120
TGCAAGGCCC	CCGCCCCTAG	TTCTCGTTCC	AGTCGTCTTC	GCACACAGGG	TGCCAGGACT	180
TCCTCTGAGA	TGAGT					195

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT	AGTGTGGCAC	ATCAGGGGGC	CATCAGGGTC	ACAGTCACTC	ATAGCCTCGC	60
CGAGGTCGGA	GTCCACACCA	CCGGTGTAGG	TGTGCTCAAT	CTTGGGCTTG	CGCCACCT	120
TTGGAGAAGG	GATATGCTGC	ACACACATGT	CCACAAAGCC	TGTGAACCTG	CCAAAGAATT	180
TTTGCAGACC	AGCCTGAGCA	AGGGCGGGAT	GTTCAGCTTC	AGCTCTCCT	TGCTCAGGTG	240
GATGCCAAC	TCGTCTANGG	TCCGTGGGAA	GCTGGTGTCC	ACNTCACCTA	CAACCTGGGC	300
GANGATCTTA	TAAAGAGGCT	CCNAGATAAA	CTCCACGAAA	CTTCTCTGGG	AGCTGCTAGT	360
NGGGGGCTTT	TTGGTGAACT	TTC				383

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 247 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:
- |   |     |
|---|-----|
| ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT | 60  |
| TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC | 120 |
| TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGCAG ANCCAGAGAC  | 180 |
| TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC | 240 |
| TGANGTC   | 247 |
- (2) INFORMATION FOR SEQ ID NO:168:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:
- |  |     |
|--|-----|
| ACTTCTAACT TTTCTAGAAC TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA  | 60  |
| AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCACTGTT TCCACAAAGG | 120 |
| GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGGC   | 180 |
| AATTCCCAAC TTCCCTGCCA CAAGCTTCCC AGGCTTCTC CCCTGGAAAA CTCCAGCTTG   | 240 |
| AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA                               | 273 |
- (2) INFORMATION FOR SEQ ID NO:169:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:
- |   |     |
|---|-----|
| ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC   | 60  |
| AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA   | 120 |
| CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG    | 180 |
| GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC   | 240 |
| CTTGCCATGG GCAAAGGCC CTACCACAAA AACAAATAGGA TCACTGCTGG GCACCAGCTC   | 300 |
| ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACACTGG | 360 |
| AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC    | 420 |
| TCGAACACTG A  | 431 |

- (2) INFORMATION FOR SEQ ID NO:170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAAGGAGCT CTGGCAGGGAT TTTCGCUAANC CCTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCCGCTAGA AAGACACCCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACGG CGAGGACTGC AGCCCCGACT CGCAGCCCTG GCAGGGCGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCCTGG TGCATCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTTCCA GAAGTGAATG CAGAGCTCCT ACACCATCGG GCTGGGCCTG	180
CACAGTCTTC AGCCCGACCA AGAGCCAGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTCGCA GTGCCCTACC	360
GCGGGGAACT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG ATAGCCTACC	420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGGAGG TCTGCAGTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAAGA GGACTCCTGC	540
AACGGTGAAT CTGGGGGCC CCTGATCTGC AACGGGTACT TGCAGGGCT TGTGTCTTT	600
GGAAAAGCCC CGTGTGGCC AGTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC	660
ACTGAGTGGG TAGAGAAAAAC CGTCCAGGG AGTTAACCT GGGGACTGGG AACCCATGAA	720
ATTGACCCCCC AAATACATCC TGCGGAAGGA ATTCAAGGAAT ATCTGTTCCC AGCCCCTCCT	780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGG CCCTCCTCCC TCAAACCAAG GGTACAGATC	840
CCCAGCCCCC CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCG TCCCTCAGAC	900
CCAGGAGTCC AGCCCCCTCT CCCTCAGACC CAGGAGTCCA GACCCCCCAGG CCCCTCCTCC	960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CCCTCCTCCC AGACTCAGAG GTCCAAGCCC	1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCAGG CCCTCTNCTC CTCAGACCCA	1080
CGGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC	1140
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTCCCC TAGATCCAGA AATAAAGTTT	1200
AGAGAAGNG CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1					5				10					15	
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
					20			25					30		
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
					35			40				45			
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly
					50			55			60				
Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu
					65			70			75		80		
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe
					85			90			95				
Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser
					100			105			110				
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe
					115			120			125				
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn
					130			135			140				
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser	
					145			150			155				

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAACGA	ATTGTTCTGC	60
TCGGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCTTGCT	CGCTAACGAC	240

CTCATGTCGA TCAAAGTGGAA CGAATCGGTG TCGGAGTGTG ACACCACTGG GGGCATCAGC	333
ATTGCTTCGGC AGTGCCTAAC CGCGGGGAAAC TCTTGCTCG TTTCTGGCTG GGGTCTGCTG	360
CGGAACTGGTGA AGCTCAACGGG TGTGTGCTG GCGTCTTCGA GGAGGTCTG TGCCCAAGTGG	410
CGGGGGGTTGAA CGCAGAGGTTGAGGTTGAA GAGAAAGGTTGAGCTG TACGGTGTG TACGGGTTGAA	470
AGCTGTGCGGT GGTGTTTGA TGGGGTTGCA GTAAAGCTTA TGACCGCTG TACCAACCCCA	540
GCATGTTCTG CGCGGGGGGA GGGCAAGGACG AGAAGGACTG CTGCAAAGGT GACTGTGGGG	600
GCCCCCTGAT CTGAAACGGG TATTTGCGAGG GCGTTGTG TTTGGGAAAA GCCCCGTGTG	660
GCGAAGTGGT CGTGGCGAGT GTTACACCA ACGCTGTGCA ATTCACTGAG TGCATAAGAGA	720
AAACCGTCCA GGCGAGTAA CTGTGGGGAA TGGGAAACCA TGAAATTGAC CGCCAAATAA	780
ATCCTCGGGAA AGGAATTCAG GAATATGTG TCGACGGCTG TCTCCNTCA GGGCGAGGAG	840
TCCAGGGCCC CAGCGCTTCA TGCTCAAAAC CAAGGGTACA GATCCCGAGC CCTCTCTCCC	900
TCAGACCCAG GAGTCCAGAC CGCCAGGCGTCTCCCTG AGACCCAGGA GTCCAGGGCCC	960
TCTCCNTCA GACCCAGGAG TCGAGACCGTCTCCCTG AGACCCAGGA CGCAGGGGTT	1020
GAGGGGGGCA ACCGCTCTC CTTCAGAAGTC AGAGGTCTAA GCCCCUAACC CCTCGTTCCTC	1080
CAGACCCAGA GGTNNAGGTC CGAGCGCTG TTCCNTCAAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTTCG CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCCAAACCTT ACCAGTTGGT	1200
TTTTCATTT TNGTCCTTT CGCTTAGATC CAGAAATAAA STTTAAAGAGA NGNGCAAAAGA	1260
AAAAAA	1285

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 174:

GGTCAGCCGC ACACTGTTTC CAGAAGTGAG TGCAGAGCTC CTACACCATE GGGCTGGGGC	40
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG	120
TACGGCACCC AGAGTACAAC AGACCCCTTGC TCGCTAACGA CCTCATGTC ATCAAGTTGG	180
ACGAATCCCT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTGCTTCG CAGTGCCCTA	240
CCCGGGGAA CTCTTGCCTC GTTTCTGGCT GGGGTCTGCT GGCAGACGGT GAGCTCACGG	300
GTGTGTGTCT GCCCTCTTCA AGGAGGTCTCT CGCCCCAGTC GCGGGGGCTG ACCCAGAGCT	360
CTGCGTCCCA GGCAGAATGC CTACCGTGCT GCAGTGCCTG AACGTGTCGG TGGTGTCTGA	420
NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACCACCC ANCAGTTCT CGCCCGGGCG	480
AGGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGG AAAGGGGAGG CCAGGGGACT	540
CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CCGCATGGCG AGATGCAGAG	600
ATGGAGAGAC ACACACGGAG ACAGTGACAA CTAGAGAGAG AAGCTGAGAG AAACAGAGAA	660
ATAAACACACG GAATAAAAGAG AAGCAAAGGA AGAGAGAAC AGAAACAGAC ATGGGGAGGC	720
AGAAACACAC ACACATAGAA ATGCAGTTGA CCTTCCAACA GCATGGGGCC TGAGGGCGGT	780
GACCTCCACC CAATAGAAAA TCCTCTTATA ACTTTTGACT CCCCAAAAC CTGACTAGAA	840
ATAGCCTACT GTTGACGGGG AGCCTTACCA ATAACATAAA TAGTCGATTG ATGCATACGT	900
TTTATGCATT CATGATATACT CTTTGTGGA ATTTTTGAT ATTTCTAAGC TACACAGTTC	960
GTCCTGTGAAT TTTTTTAAAT TGTGTCAACT CTCCCTAAAT TTTTCTGATG TGTGTTATTGA	1020
AAAAATCCAA GTATAAGTGG ACTTGTGCTAT TCAAACCGAG GTTGGTCAAG GGTCAACTGT	1080
GTACCCAGAG GGAACACGTG ACACAGATTC ATAGAGGTGA AACACGAAGA AAAACAGGAA	1140
AAATCAAGAC TCTACAAAGA GGCTGGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTTT	1200
CCGAGGGAG GCACCCAGAT CACTTGACGT AACCACTTCAG AGACCAACCT CGCCAAAATG	1260
GTGAAATCCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGGCTGT	1320
AATCCCGAGCT ACTTGGGAGG CTGAGGGCAG AGAATTGCTT GAATATGGGA CGCAGAGGTT	1380
GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGG AACAGAGTAA GACTCTGTCT	1440
CAAAAAAAAAA AAAAAAAAAA	1459

## (2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCCTA	CACCATCGGG	120
CTGGGCCTGC	ACAGCTTGTA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GSCACCAGA	GTACAAACAGA	CTCTTGCCTC	CTAACGAACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCCCTGCA	ACCGTGACTC	TGGGGGGCCC	CTGATCTCCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTTCG	AAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CAACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATAACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCC	720
GCCCCTCCTC	CCTCAGGCCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CACACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TGNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTG	CCTTTCCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Vai	His	Pro	Gln	Trp
1									10						15

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
									20						25

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
								35							40

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Leu	Leu	Leu
								50							55

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 60 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Glu Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met  
 100 105 110  
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val  
 115 120 125  
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala  
 130 135 140  
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly  
 145 150 155 160  
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys  
 165 170 175  
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys  
 180 185 190  
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACTCGC	AGCCCTGGCA	GGCGGCACTG	GTCATGGAAA	ACGAATTGTT	CTGCTCGGGC	60
GTCCTGGTGC	ATCCGCACTG	GGTGTGTCA	GGCGCACACT	GTTTCCAGAA	CTCCTACACC	120
ATCGGGGCTGG	GCCTGACAG	TCTTGAGGCC	GACCAAGAGC	CAGGGAGCCA	GATGGTGGAG	180
GCCAGGCCTCT	CCGTACGGCA	CCCAGAGTAC	AACAGACCCCT	TGCTCGCTAA	CGACCTCATG	240
CTCATCAAGT	TGGACGAATC	CGTGTCCGAG	TCTGACACCA	TCCGGAGCAT	CAGCATTGCT	300
TCGCAGTGCC	CTACCGCGGG	GAACTCTTG	CTCGTTCTG	GCTGGGGTCT	GCTGGCGAAC	360
GATGCTCTGA	TTGCCATCCA	GTCCCCAGACT	GTGGGAGCT	GGGAGTGTCA	GAAGCTTTCT	420
CAACCCCTGGC	AGGGTTGTAC	CATTCTGGCA	ACTTCCAGTG	CAAGGACGTC	CTGCTGCATC	480
CTCACTGGGT	GCTCACTACT	GCTCACTGCA	TCACCCGGAA	CACTGTGATC	AACTAGCCAG	540
CACCATAGTT	CTCCGAAGTC	AGACTATCAT	GATTACTGTG	TTGACTGTGC	TGTCTATTGT	600
ACTAACCATG	CCGATGTTA	GGTCAAATTA	GGCTCACTTG	GCCTCAACCA	TCTTGGTATC	660
CAGTTATCCT	CACTGAATTG	AGATTTCTG	CTTCAGTGTG	ACCCATTCCC	ACATAATTTC	720
TGACCTACAG	AGGTGAGGG	TCATATAGCT	CTTCAGGAT	GCTGGTACTC	CCCTCACAAA	780
TTCATTCTC	CTGTTGTAGT	GAAAGGTGG	CCCTCTGGAG	CCTCCCAGGG	TGGGTGTGCA	840
GTCACAATG	ATGAATGTAT	GATCGTGTTC	CCATTAA	AAGCTTTAA	ATCCCTCATG	900
CTCAGTACAC	CAGGGCAGGT	CTAGCATTTC	TTCATTTAGT	GTATGCTGTC	CATTCAATGCA	960
ACCACCTCAG	GAATCCTGG	TTCTCTGGCT	AGTTGAGCTC	CTGCAATGCTG	CCTCCTTGGG	1020
GAGGTGAGGG	AGAGGGCCCA	TGGTTCAATG	GGATCTGTGC	AGTTGTAACA	CATTAGGTGC	1080

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

## (2) INFORMATION FOR SEQ ID NO:178.

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			
Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
	20						25				30				
Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
	35				40					45					
Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
	50				55				60						
Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
	65				70			75				80			
Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
	85						90				95				
Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
	100				105						110				
Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
	115					120				125					
Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
	130				135				140						
Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
	145				150				155				160		
Pro	Gly	Thr	Leu												

## (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60

110

CCAGGTGCCC CGGGCGGGG GATGGAGGC TCGAGGAAAC CTTGCCGGC TGTGATTGCT	170
GGCAAGGCACT GTTCATCTCA CCTTTCTGT CCCCTTGCTC CGGCAAGGG CTTCCTGCTGA	180
AAGTTCATAT CTGGACCCCTG ATGCTTAAT GAATAAGCT CCCATCTTC ACCCCCCAAA	240
AAAAAAAAAA	250

## (2) INFORMATION FOR SEQ ID NO:180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTG CGCGTGCCTC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTCTACT CGGAAACTAT TTTTATGTAA TTAATGATG CTTCTTGTT TATAATGCC	180
TGATTTAAAA AAAAAAAAAA AA	202

## (2) INFORMATION FOR SEQ ID NO:181:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTAGG CAGTGTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTTCTGAA GATTAATGAA GTGAAAATT GAGGTGGATA AATACAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTTGGCTAG AAAAAATTAT AACACAGGACT TTGTTAGTTT GGGAGCCAA	360
ATTGATAATA TTCTATGTC TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420
TTTATTCCCC AGGAATATGG KGTTCATTTT ATGAATATTA CSCRGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGTTT GACTTATTTC	540
CAAAAAAAAAA AAAAAAAAAA	558

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCCGA RWTYGTTTGA TCCAACCCCTG CCTTWTTTTC	60
AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCCTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTG ACGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGIGATG TCCCTAGTCA	240
CTAAGGTTAA ACTTTCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTTCTA AGTCTCTTC CAGCTCACT KKGAGTCCTM CYTGGGGTT GATAGGAANT	360
NTCTCTTGCG TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGAG TACGCTARA	420

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAA AAAA AAAAAAAA 479

## (2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGCTAAA	GCCAAAGCCC	AAGAACAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAAGTA	CCAATAACAG	TGCCAGTGCC	AGTGCCAGCA	CCAGTGGTGG	120
GGTGCAGGCC	TGACCGCCAC	TCTCACATT	GGGCTCTTCG	CTGGCCTTGG	180
GCCAGCACCA	GTGGCAGCTC	TGGTGCTGT	GGTTTCTCT	ACAAGTGAGA	240
TGTTAACCT	CCCAGTCTTT	CTCTTCAAGC	CAGGGTGCAT	CCTCACAAAC	300
CAGCACTCTA	GGCAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	360
GGCATTTCAA	AAAAA	AAAAA			384

## (2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC	TTATAAGCGA	TCATGTYNT	CCRGTATKAC	CTCAACGAGC	60
AGGGAGATCG	AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAAACAG	120
CCCATCTGC	TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAAC	180
AAAGCTTCA	GGTGCTCATG	ACCCAGCAAC	CGCGCCCTGT	CCTCTGAGGG	240
TGATGTC	TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	300
TGAGCCCTGA	TGCCTTTTG	CCAGCCATAC	TCTTGCGAT	CTTCGGACTG	360
ATTATGCTTG	TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	420
TTTTCTCAT	ATTTAAATT	ACTACMAGAW	TATTW MAGAW	WAAATGAWTT	480
AAAAAAAAAA	AAAAA				496

## (2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGGGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGRAC	AGTGACTTCC	60
CAAGTATCYT	CGCGSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTCCGG	120
AGGAGGACAT	GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTCGGAG	180
GGGCACACCC	TCTCTGGGCC	CAGGGGGCA	CCTGCGTCTC	CCAGTATGCC	240
TGGTGCTGCT	CCTCGTCATC	TTCTGCTCG	TGGCCAACAT	AACTGGCTGG	300
TTGCCATGTT	CAGTTACACA	TTCCGGCAAAG	TACAGGGCAA	CAGCGATCTC	360
GCGCAGCGTT	ACCGCCTCAT	CCGG			384

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCTGGCA	TCTTGGGGG	GCNTAAATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCCTCCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTTGTACCAG	CTCTCTGACA	GTGAGGTAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTGCAGA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAG	ACATTGACAA	ACTCGCCAG	420
GTGGAAAAAAAG	AMCAMCTCCT	GGARGTGCTN	GCCGCTCTC	GTCMGTGGT	GGCAGCGCTW	480
TCCTTTGAC	ACACAAACAA	GTAAAGGCA	TTTCAGCCC	CCAGAAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAAT			577

## (2) INFORMATION FOR SEQ ID NO:187:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAAATAT	CGATCCGATN	TTGTCGTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTCAACAT	ATGCAACACT	120
TTAACACGTG	TGTCAATCTG	CTCCCCYNAC	TTTGTATCA	CCAGTCTGGG	AKAAAGGGTA	180
TGCCCTATTC	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTGTA	GCGGAAGAGT	AGCCTTCTA	CTTCACCAGA	CACAACCTCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATTAA	CCACTTGCAC	AAGAAGGCGT	TTTCTTCCTC	AGGC	534

## (2) INFORMATION FOR SEQ ID NO:188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TCTCTCCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTTT	TACTTTGTG	AAAGCTTATG	120
CCTCTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTC	TCTAGTTNGT	240
TTTATTGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKTT	WTCTCCCTT	420

GCAAAAAAACA TGTACNGACT TCCCCTTGAG TAATGCCAAG TTGTTTTTTT TATNATAAAA	480
CTTGCCTTC ATTACATGTT TNAAAGTGGT GTGGTGGGCC AAAATATTGA AATGATGGAA	540
CTGACTGATA AAGCTGTACA AATAAGCACT CTGCTTAACA AGCAACACAC TAATCTTGAC	600
ATGCCTTAATT CACAAATGCT AATTTCATTA TAAATGTTG CTAAAATACA CTTTGAACCA	660
TTTTCTGTN TTCCAGAGC TGAGATNTA GATTTATGT AGTATNAAGT GAAAANTAC	720
GAAAATAATA ACATTGAAGA AAAANANAAA AAANAAAAAA A	761

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTT TTTGCCGATN CTACTATTT ATTGCAGGAN GTGGGGGTGT ATGCACCGCA	60
CACCGGGGCT ATNAGAAGCA AGAAGGAAGG AGGGAGGGCA CAGCCCCCTG CTGAGCAACA	120
AAGCCGCCTG CTGCCTTCTC TGCTGTCTC CTGGTGCAGG CACATGGGGA GACCTTCCCC	180
AAGGCAGGGG CCACCAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG	240
TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCA	300
GTCATTGTGC CCTGCCAGG CACAGCGTAN ATCTGGAAAA GACAGAATGC TTTCCCTTTC	360
AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTNG GCTNGGTCTT GGTACNCTTG	420
GTTCGGCCA GCTCCNCGTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCNGGNCCC	480
CC	482

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTT TTTAAAACA GTTTTCACA ACAAAATTAA TTAGAAGAAC AGTGGTTTG	60
AAAACCTCTG CATCCAGTGA GAACTACCAT ACACCCACATT ACAGCTNGGA ATGTNCTCCA	120
AATGTCTGGT CAAATGATAC AATGGAACCA TTCAATCTTA CACATGCACG AAAGAACAAAG	180
CGCTTTTGAC ATACAATGCA CAAAAAAAAGGGGGGGGG GACCACATGG ATAAAAATT	240
TAAGTACTCA TCACATACAT TAAGCACAG TTCTAGTCCA GTCAAAATC AGAACTGCNT	300
TGAAAATTT CATGTATGCA ATCCAACCAA AGAACTTNAT TGGTGATCAT GANTNCTCTA	360
CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAA ANCACNCNGT AAAAAANAA	420
TCTGTAATTN ANTTAACCT CCGTACNGAA AAATNTNNNT TATACACTCC C	471

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTTC TASTGTCGGM CTGTTAGCC ACCAACTCTA ACAAGTTCT	60
GTCTTCCACT CACTGTCTGT AAGCTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA	120

ATTCCTTCAAC	AGTCACATCT	TCTAGGACCT	TTTGATTG	AGTTAATATA	AGCTCTTCCA	180
CTTCCTTGT	TAAGACTTCA	TCTGGTAAAS	TCTTAAGTTT	TGTAGAAAGG	AATTYAATTG	240
CTCGTTCTCT	AACAAATGTC	TCTCGTTGAA	GTATTTGCT	GAACAACCC	CCTAANGTCC	300
CTTTGTGCAT	CCATTTAAA	TATACTTAAT	AGGGCATTGK	TNCACTAGGT	YAAANTCGCU	360
AAGAGTCATC	TGTCTGCAA	AGTTGCCTTA	GTATATGTGC	CA		400

## (2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCCGAT	CCAATAATCT	TTGCTCTGAGC	GCACCACACA	TATNCACTCC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTGTGGA	AAAACCTGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCATT	GCTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTTGCC	TCCATCACAT	TTGTGATCTC	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTGTGTT	CAAAGCARC	TCTTGGTGCC	420
TGTTGGATCA	GGTCCCATT	TCCCAGTCYG	AATGTTTCACA	TGGCATATTT	WACTTCCCAC	480
AAAACATGC	GATTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAAGCA	600
G						601

## (2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 608 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCCA	NATCCCACCA	CGAACGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACCCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACCTCCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTCCAG	GAAGAGGCTG	ACCACCTCGC	GGTCCACCAAG	GATGCCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GGCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCCAAGTG	TGTCGGCCTC	420
CAGGAMMGSC	ACCACGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGGCCCTG	CGTGAGCAGC	ATGAAGGCGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

## (2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAGGCAGYT	60
CCAGTCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCGCTCT	GGCCCTTCCCC	120
TCCGCCTCAA	TCCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAACGA	GTGAACACTG	180
TTTGATTTTA	CTTGGGAATT	TCTCTGTAA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAC	240
AACAACAACA	AAATAACATG	TTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAGAGAAAT	ATTACTGTAA	CATATACTGC	TTGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCAAC	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAAGGC	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCCTCTCA	GTCCCCCTCC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCCG	CCATGGGGAR	TGTGCTCAAG	GARTCGCNNG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAAA	AAAAANAAAAA	AA				502

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCAT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTTGTAACT	360
TCACTTGGTT	ATTTTATTGT	AAATGARTTA	CAAAATTCTT	AATTAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATT	CTTCCTKG	TTACGTTAAT	TTTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTGTAGAAT	GTATAAAGGT	TGTAGCCCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTATAA	ACTAGCAAAN	660
	AAGTG					665

## (2) INFORMATION FOR SEQ ID NO:197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTTNTTTT	TTTTTTTG	AGGAAGGATT	CCATTATTG	TGGATGCATT	TTCACAAATAT	60
ATGTTTATTG	GAGCAGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	CATNAGAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAAATGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAG	300
ATTCTCTCT	GAACCTTACA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATE	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTTT	CTTCATNCTC	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTG	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGCCAN	GAGAAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTC	TGTCACTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGT	CGGACTTTGA	180
AGTGATTCA	TTTCCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTTA	360
ANGGACTTIA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCNNG	CCGTTTANTG	420
AACNTNGACN	NCACCCCTNT	GGAATANANT	CTTGACNGCN	TCTGAACTT	GCTCCTCTGC	480
GA						

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200.

CGGGGGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCC	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGA	GAGGTCTGTG	CACGTCCCAC	GACCTTGACG	CCGTCGGGA	180
CACCCCGAAC	AGAGCCCGGT	GAANGCGGG	GGCCTCGGG	AGCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CCGAGGTGCA	GGTGGCCGCC				270

## (2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTT	TTTGAATC	TACTGGGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTCTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAANCGAAC	ANAANTAA	180
TGGAGTGGGT	GCACCCCTCC	TGAGAACCT	GGTTACNAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANAAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNCAATAAC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	60
TGGCACTTAA	TCCATTTTA	TTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATAACNG	120
GTNATTTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAAA	AATCAAAAT	ATACNTNTCT	TTCAGCAAAC	TTNGTTACAT	AAATTAAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTTNNAA	300
GGAACAAAAA	AAAAAAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAAACAACAA	ATTCTNTTTA	360
CAACANCNC	NATTAAAAAA	ATCATATCTC	AAATCTTAGG	GGAAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTACTNCA	CTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAAACA	480
CAATGGNAAT	NCCNCCNCC	TGGACTAGT				509

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTGA	GGCGCCTCTT	ATAAAAACA	AGTTACATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGSTATTA	ATATTCAAA	GGCAGCTTT	AAAATCAAAC	120
TAATGGAAA	CTGCCTTAGA	TACATTAATC	TTAGGAATTA	GCTTAAAATC	TGCCTAAAGT	180
AAAAATTTTC	CTAGCTCTT	TTGACTGTAA	ATTTTIGACT	CTGTAAAAC	ATCCAAATTC	240
ATTTTTCTTG	TCTTAAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTGG	AAGTCAATTT	300
GETTCTCTAG	CCTCATTCC	TAGETCTTAT	CTACTATTAG	TAAGTGGCIT	TTTCCTAAA	360
AGGGAAAACA	GGAAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTJTGAGGC	AGCTCAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTCTAG	TCACTAAACG	ATAICNAAAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATTT	540
ATTCAAAAGC	TAATATAAGA	TATTTTACAT	ACTCATCTTT	CTG		58?

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTCTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAA	CTCATCTTC	CAGCTTTAAA	ATAACAATCA	120
AAATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTTCTCC	180
TGAAGGAAAT	CTGTCATTC	TTCTCATCCA	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	TCAAACCTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTCCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAA	CTGCTCAAAT	TGTTTGTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTTAC	NGACNAGCAA	TAATAAAACT	GAAGTACCAAG	TTAAATATCC	480
AAAATAATTA	AAGAACATT	TTTAGCCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCACA	TGTTATTATT	CCNTAGCCC	ACACAATGG		589

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT	TTTTTTCAGT	AATAATCAGA	ACAATATTTA	TTTTTATATT	TAAAATTCTAT	60
AGAAAAGTGC	CTTACATTAA	ATAAAAGTTT	GTTCCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGCTTGAA	CACCAATATT	AATTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTAAAAAGA	TTAAATTGTA	CCTCAGAAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAA	AAATTACTA	TGGACTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGT	ACTGGTAAAC	CAACACATTC	TGAACGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTTGACAAAGT	TCTCTTTCT	TCAATCTTT	420
AAGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TTGCCAATAT	TAAGAAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

## (2) INFORMATION FOR SEQ ID NO:206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTAGTC	AAGTTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTTATTAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTTNTTAG	ACAACGTNA	120
CAATTTATAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGCAA	ACGCTAACCT	TCTTCTCCAT	CCCCATGTNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGCCTT	360
TCGGTAAAAA	TAGACTGTGT	CTGTCGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAAA	60
TACATAGCAT	AAAATCCCAA	ATCCTATTAA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTTCGAT	GCAGAGGAGG	AAAAGGTAT	TGGATTTCGA	CAGAGGAANA	ACACAGCGCA	240
GAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAACGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTAA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTGGCAGAA	TACTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCAAA	300
GTAAATAGAA	GTGGGTATA	ATATTAATTA	CCTGTTACAA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCACTAGA	CAGGAGGCTG	TCACCTTGCAC	CAAATTCTCA	CCAGTCATTC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACTTGTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA	159

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAGTGCC	60
ACTGAATTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA ACCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTT GATTGTCAA	60
CGATTTAATC TTGTCCTCAGC TTGGCCACTT CAGTTAGGAC CTAACCATGC CAGCCCCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCC CGACAACAGG TTATTCAGT TGCCCCGCCAG	180
TTNAATTTCAT TTCCCATTGA CTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCTTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA	300
TTTTTTTTTC CTTTATTTCCT TTGTCAGA	328

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACGTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTG ATTGTCAAAG	60
GATTTAATGT TGTCTCAGCT TGGGCACCTTC AGTTAGGACC TAAGGGATGCC AGCCGGCAGG	120
TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACCTT GCCCGCCAGT	180
TGAATTTCAT TCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC	240
CCCTTACGACT CTTTACTCTC TGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT	300
TTTTTTTTCC TTTATTCCTT TGTCAAGAGAT GCGATTTCATC CATATGCTAN AAACCAACAG	360
AGTGAACCTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT	420
ACTTTGCTCT CCCTAATATA CCTC	444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAACGTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120

CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TOTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT	240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGJACCATA GCGAANAAAA AACTTAGTAA	100
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTGTAACCAA GGTGGAAATC TGTATACTT	260
GGTGCC	366

## (2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 260 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC	60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNNTAA GGCTNTTNC ATTTTTTTAT	120
TAATAAAAAG TNAAAAGGC CTCTTCTCAA CTTTTTCGC TTNGGCTGGA AAATTTAAAA	180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT	240
AATTCTTCCT TCCCTCCTT	260

## (2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCTAT AATTTCTAT TTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTA	120
GGCATTCTAC AGTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GACTAGATT ATAATTAGCC ACTTACCC	210
ATATCCTCTA TGCTTGTAAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCCTA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGGA TTCCATGAGG	60
TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

ACCCCGCTCGT CGGGAGGGCG GTACTGACCT CATTACTAGG AGCATGCCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATAAAAA AAATTAATAA TGAATTTTG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT	300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT CGTATTATTG TATTGATAAG T 351

## (2) INFORMATION FOR SEQ ID NO:223

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTTC CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAAA TTTTGATTTT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCAGAGGA AGTCTAAGGA ATTACTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATTG	240
TAAAAGATTT TGATTTCTG GAATGACAAT TATAATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG	360
ACCATTAAGC TATATGTTA AAA	383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereto, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : C12N 15/12, C07K 14/705, C12N 5/10, 1/21, A61K 38/17, C12N 1/19, A61K 39/00, C12N 15/62		A3	(11) International Publication Number: <b>WO 98/37093</b>
			(43) International Publication Date: 27 August 1998 (27.08.98)
(21) International Application Number: PCT/US98/03492		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 25 February 1998 (25.02.98)			
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(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).			
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).			
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).			
<p><b>Published</b>  <i>With international search report.</i>  <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>			
(88) Date of publication of the international search report: 17 December 1998 (17.12.98)			
<p>(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE</p> <p>(57) Abstract</p> <p>Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.</p>			

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<b>DK</b>	Denmark	<b>LR</b>	Liberia	<b>SG</b>	Singapore		
<b>EE</b>	Estonia						

**INTERNATIONAL SEARCH REPORT**

International Application No
PCT/US 98/03492

A. CLASSIFICATION OF SUBJECT MATTER					
IPC 6	C12N15/12	C07K14/705	C12N5/10	C12N1/21	A61K38/17
	C12N1/19	A61K39/00	C12N15/62		

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---	
A	WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document ---	
A	WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document ---	
A	EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document ---	
		-/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

\* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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- "Z" document member of the same patent family

Date of the actual completion of the international search

30 July 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA

European Patent Office, P.O. Box 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,  
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Authorized officer

Oderwald, H

## INTERNATIONAL SEARCH REPORT

Inten	nal Application No
PCT/US 98/03492	

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES" NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597 see the whole document &amp; "AC No. AA453562" EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765</p> <p>---</p>	2,4-6
X,P	<p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)" EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072</p> <p>see the whole document</p> <p>-----</p>	2,4-6

## INTERNATIONAL SEARCH REPORT

Int. application No

PCT/US 98/03492

### Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:  
Remark: Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2.  Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3.  Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1.  As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4.  No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

#### Remark on Protest

- The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 15.
11. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 16.
12. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 17.
13. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 18.
14. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 19.
15. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 20.
16. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 21.
17. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 22.
18. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 23.
19. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 24.
20. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 25.
21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 26.
22. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 27.
23. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 28.
24. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 29.
25. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 41.
26. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 42.
27. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 43.
28. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 44.
29. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 45.
30. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 47.
31. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 48.
32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 49.
33. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 50.
34. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 51.
35. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 52.
36. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 54.
37. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 55.
38. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 56.
39. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 57.
40. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 58.
41. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 59.
42. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 60.
43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 61.
44. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 62.
45. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 63.
46. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 64.
47. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 65.
48. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 70.
49. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 73.
50. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 74.
51. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 79.
52. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 81.
53. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 87.
54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 90.

55. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 92.

56. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 93.

57. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 97.

58. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 103.

59. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 104.

60. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 107.

61. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 109.

62. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 110.

63. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 111.

64. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 115.

65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 116.

66. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 117.

67. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 118.

68. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 119.

69. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 120.

70. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 121.

71. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 122.

72. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 123.

73. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 124.

74. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 125.

75. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 126.

76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 138.
88. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 139.
89. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 140.
90. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 141.
91. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 142.
92. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 143.
93. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 144.
94. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 145.
95. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 146.
96. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 147.
97. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 148.
98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 152

102. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 155.

105. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 156.

106. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25  
same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

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same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially  
same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 6.

133. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 7.

134. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 30.

135. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 31.

136. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 32.

137. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 33.

138. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 34.

139. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 35.

140. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 36.

141. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 37.

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142. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 38.

143. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 39.

144. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 40.

145. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 46.

146. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 53.

147. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 66.

148. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 67.

149. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 68.

150. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 69.

151. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 71.

152. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 72.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

153. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 75.

154. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 76.

155. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 77.

156. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 78.

157. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 80.

158. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 82.

159. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 83.

160. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 84.

161. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 85.

162. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 86.

163. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 88.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

164. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 89.

165. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 91.

166. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 94.

167. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 95.

168. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 96.

169. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 98.

170. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 99.

171. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 100.

172. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 101.

173. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 102.

174. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 105.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

175. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 106.

176. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 161.

177. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 162.

178. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 163.

179. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 164.

180. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 165.

181. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 166.

182. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 167.

183. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 168.

184. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 169.

185. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 170.

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186. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 179.

187. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 180.

188. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 182.

189. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 183.

190. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 184.

191. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 185.

192. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 186.

193. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 187.

194. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 189.

195. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 190.

196. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 192.

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197. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 195.

198. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 196.

199. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 197.

200. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 199.

201. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 200.

202. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 201.

203. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 202.

204. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 205.

205. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 206.

206. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 208.

207. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 212.

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208. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 213.
209. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 214.
210. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 215.
211. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 216.
212. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 217.
213. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 218.
214. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 219.
215. Claims: 12-18 all partially  
same as invention 131 but for SEQ ID NO: 221.

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